

```
QY 806 AYKGLLVGVYMAWETRHVKIPALNDSOYIGVSVSWITSAIVVLANLISERVTLAF 865
Db 661 aykgllmlfgcfiawetrnvsipalndskyigmvynvgimciigaavsfldrqpvnqf 720
QY 866 ITITALILTSTTATLCLFLTPKLDIWARNDIIDPVIHSMGLKMECNTRRFVVDRLQ 925
Db 721 civalvliifcsttitclvfpkl-----itlrtpdaatqnrfrq 760
QY 926 YRVEVONRVYKKEIQALDAEIRKLERLLESGLTSTTT--SSSTSLLTG----GGHLKP 979
Db 761 f---tqng--kk-----edsktstsvtsvnqastsrleglqsenhrirm 799
QY 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011
Db 800 kitelkdleevcmqldtpekttyikqnhyqelndillsignfctestdggkailknhl-- 857
QY 1012 VLPPVIPRASWPSAE 1026
Db 858 ----dppqlqwnnte 869
```

Search completed: April 30, 2002, 10:00:46
Job time: 589 sec

Db 661 aykglmlfclawetrvnsipalndskylgmsvynvgimciigaavsfllrtdqnvqf 720
QY 866 ITITALLTSTATLCLLFIPKLDHIDWANDIIDPVIHSMGLKMECNTRFRFVVDREELQ 925
Db 721 civalviifcstlclvfpkl-----itlrtpdaatqurrfq 760
QY 926 YRVEQNVYKKEIQALDAEIRKLERLLESGLTTTSTYT---SSSTSLLTG-----GGHLKP 979
Db 761 f---tqnq--kk-----edsktstsvtsvndqastsrleglqsenhrlrm 799
QY 980 ELT-----VTSGISOTPAASK-----NRTPSISG---ILPNLLLS 1011
Db 800 kiteldkdvtnqldtpektikqnhqyelndilslgnftestdggkailknhl-- 857
QY 1012 VLPPIPRASWPSAE 1026
Db 858 ---dqpqlqwnite 869
RESULT 15
AA770327
ID AAY70327 standard; Protein; 940 AA.
XX AAY70327;
XX 21-JUN-2000 (first entry)
XX Rat gamma amino butyric acid receptor, GABA-B-R2 protein.
XX Gamma amino butyric acid; GABA-B-R2; rat; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antiasthmatic; antiaddictive;
KW uropathic; analgesic; antitussive; agonist; neuroprotective; nootropic;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX Rattus sp.
XX Key Location/Qualifiers
FH Peptide 1..40
FT /label= Signal_peptide
FT Protein 41..940
FT /label= Mature_rat_GABA-B-R2_receptor_protein
FT Domain 480..503
FT /label= Transmembrane_domain-I
FT Domain 517..544
FT /label= Transmembrane_domain-II
FT Domain 555..577
FT /label= Transmembrane_domain-III
FT Domain 596..618
FT /label= Transmembrane_domain-IV
FT Domain 654..676
FT /label= Transmembrane_domain-V
FT Domain 690..711
FT /label= Transmembrane_domain-VI
FT Domain 719..743
FT /label= Transmembrane_domain-VII
XX WO200012692-A1.
XX 09-MAR-2000.
XX 27-AUG-1999; 99WO-US19651.
XX 27-AUG-1998; 98US-0141760.
PR 16-OCT-1998; 98WO-US22033.
PR 04-NOV-1998; 98US-0186664.
PR 15-DEC-1998; 98US-0211755.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX Jones KA, Laz TM, Borowsky B;
XX

DR WPI: 2000-246751/21.
XX N-PSDB; AA251400.
PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
PT detecting receptor agonists useful for treating e.g. asthma,
PT incontinence, and Alzheimer's disease -
XX Claim 12; Fig 4; 260pp; English.
PS The present amino acid sequence is the rat GABA (gamma amino butyric
CC acid)-B-R2 receptor protein, isolated from rat hypothalamic cDNA library.
CC This sequence is used to construct the plasmid BO-55 (ATCC.No. 209104).
CC GABA-B is a major inhibitory neurotransmitter, the receptors of which are
CC widely distributed throughout the central nervous system. GABA-B-R2
CC receptor has anticonvulsant, antiasthmatic, uropathic, analgesic,
CC antitussive, antiaddictive, nootropic and neuroprotective activity.
CC GABA-B-R2 receptor agonists may be used to treat spasticity, asthma,
CC incontinence, drug addiction, Alzheimer's disease, decrease nociception
CC and as an antitussive agent. Transgenic animals with altered GABA-B-R2
CC levels may be used to determine the physiological effects of varying
CC levels of GABA-B-R2 receptor activity.
XX Sequence 940 AA;
SQ Query Match 15.9%; Score 1065.5; DB 21; Length 940;
Best Local Similarity 29.5%; Pred. No. 1.6e-85;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;
QY 155 LLGLFELSTGRPPDGLSELGAATMAVEHINRRRLPGYTELVNTDQDPCGVGVDRF 214
Db 57 imglmpitkeavagsigrvlpavelaleqirneslirpyfldrllydtecdnqykaf 116
QY 215 FHAIYTOPSTRMVMLLGACSEVTESIAKVVPYNNIVQVSGTSPALSDRREPEFYRT 274
Db 117 ydaikygn--hlmvfggvcpvstiaeslqgnlvqlsfaatpvladkkyppfirt 174
QY 275 VAPDSSHNPARIAFIRKFGWGTVTTFQSENEVHSLAVNNLVLEAANISCAAITFA-- 332
Db 175 vpsdnavnpaillklkhfrwrrvgtltqdvqrfsevrndltgvygdieisdesfnd 234
QY 333 -ATDFKQLLLRLRTDTRIIGSFQSQELAPOILCEAVRLRMFGADYAWILHESGAPWMP 391
Db 235 pctsvkk---lkgndvriilqgfdqmaakvfccaeesmfkskyqvygwypawwe 290
QY 392 D----QRTACSNHQLAVENLIIVSTHNSIVGNVNNVSYSGLNNHMFNSQLRKSAQPHG 446
Db 291 qvhveansrclrrsliaamegyi-----gvdfepllskqiktisgktpqgyer 339
QY 447 Q-DGFGSGYGPRIISAATQSDSRRRRRRVVGTSGGHLFPEAISOYAPQTYDAVMAIALA 505
Db 340 eynskrsgvvp-----skfhgavydgiwviakt 367
QY 506 LRAAEHRRNEBOSKLDGFDYTRSDMAWEFLQOMGLHLFLGVSGPVSFSGPDRVGTTFAT 565
Db 368 lgrametlhassrhqrigdfnytdhtlqkiilnamnetnffgvtgqvvrngermgtikf 427
QY 566 YQIQGLLEPVALYYPATDALDFRCPRCPVPKWHSGQVPIAKRVFKLRVATIAPIAFYTI 625
Db 428 tqfqsrevkvgeynavadtleiind---tirqfsgseppkdktilleqlrkisiplyail 484
QY 626 ATLSVGIALAITFLAFNLHFKLKAIKLSSPKLSNITAVGCIFFYAPVILLGDHSTLP 685
Db 485 saltilgmimasafllfnknrqnqllkmsppymnnlililggmlisyasifilfdgsfv- 543
QY 686 SAEDSFATVCTARVYLLSAGFSIAFSGNFAKTYRVHRIFFTRTSGVFKDKMLQDILILLY 745
Db 544 -sektfetlctvrtwiltvgyttafmgafaktwrvaifknv--kmmkikiqdkllviv 600
QY 746 GGLLLVDALLVTLWVTDPMERHHLNLTLEISATDRSVVYQPOVEKRSQHTWLSVLY 805
Db 601 ggmlldilclilicwqavdprrrtverysmepdpagrdisrpllehcenhtmtlwgiv 660


```
QY 155 LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKRLLPGYTLLELVNTDQCPCGVGVDRF 214
Db 58 imglmlptkevaksigrvlpavelaleqirnesllrpyfldrlrlydtecdnakglkaf 117
QY 215 FHAIYQTPSTRMVMMLGSGACSEYTESLAKVVPYNNIVQVSGFSTSPALSDRRREPFYFRT 274
Db 118 ydaikygnp--hlmgvggpcsvtsiaeslqgnwlvqlsfaattpvladkkykpyffrt 175
QY 275 VAPDSHNPARIATFRKFGWGTVTTSQNEEVHSLAVNNLVTELEAANISCAATITFA-- 332
Db 176 vpsdnavnpaillklkhgwkrgvtltqdvrfsevrndltgvygedleisdstesfnd 235
QY 333 -ATDFKEQLLLRETDRIIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
Db 236 pctsvek--lkgndvriilqgfdqnnmaakvfccayeenmygkyqwiipwyepswwe 291
QY 392 DQRT-----ACSNHELQLAIVENLIVVSTHNSIVGNVSYSLNNHMFNSQLRKQSAQFHG 446
Db 292 qvhteanssrrclrknl laamegyi-----gvdfeplesskqiktsgktqpqyer 340
QY 447 Q-DGFGSGYGPRIATAATQSDSRRRRRRVGVGTSGHLFPPEAISQYAPQYDAVWAIALA 505
Db 341 eynnkrgvgp-----skfhgyaydgivwiakt 368
QY 506 LRAAEHWRNREEQSKLDGFDYTRSDMAWEFLQMGKHLHFLGSGVPVSFSGPDRVGTAF 565
Db 369 lgramethlhasrhqridqfnydhtlgrilnamnetnffgtgvvfrngermgtikf 428
QY 566 YQIQRGLEPVALYYPATDALDFRCPRCPVKWHSQGVPTAKRVEKLRVATIAPLAFYTI 625
Db 429 tqfqsrevkvgeynavadtleind---tirfgseppkdkilleqlkislplysli 485
QY 626 ATLSVVGIALAITFLAFNHLFRKLKAIKLSPPKLSNITAVGCIIFYAVTIVLLGDHSTLP 685
Db 486 saltlglmmasafllfniknrnqklkmspsymnnliilgmslasyasiflfigdgsfv- 544
QY 686 SAEDSFATVCTARVYLLSAGFLSAGFMAKTYRVHRIFTRTGSVFKDKMLQDQLLILV 745
Db 545 -sektfeticlvtwltvgtytafgamfaktvrhvaifknv--kmkkkikdklliv 601
QY 746 GGLLVADALLVTLVWVTPMERHLNLTLEISATDRSVYQPOVEVCRSQTOTWLSVLY 805
Db 602 gmlldilclicwqavdplrtvkeysnepdgrdisirpilehcenthmtiwigivy 661
QY 806 AYKGLLLVGVYMAWETRHVKIPALNDSQYIGVSVYSVWITSATVAVVLANLISERVTLAF 865
Db 662 aykglmlfclawetrvnsipalndskiygmsvynvgimcligaavsftrdqpvnqf 721
QY 866 IITAILITSTATCLLPIPKLHDITWARNDIIDPVIHSMGLKMECNTRFRVVDRELQ 925
Db 722 civalvifcstltclvfvpl-----itlrtnpdaatqnrfq 761
QY 926 YRVEQNVYKKEIQALDAIEKRLERLLESLGTLTTSTT--SSSTSLLTG---GGHLKP 979
Db 762 f---tqnq--kk-----edsktstvsvngaststleqlqsenhrlrm 800
QY 980 ELT-----VTSGISQTPAASK-----NRTPTISG---ILPNLLLS 1011
Db 801 kiteidkdelevtmqlqdpekttyikqnhyqelndilnlnfnftestdgkailknhl-- 858
QY 1012 VLPPIVPRASWPSAE 1026
Db 859 ---dqnpqlqwnnte 870
RESULT 12
AAB50088
ID AAB50088 standard; Protein; 941 AA.
XX AC
XX AAB50088;
XX AC
XX DT
XX 19-MAR-2001 (first entry)
```

```
DE HG20 protein sequence.
KW Human; HG20; gamma-amino-butyric acid receptor; GABA-B.
OS Homo sapiens.
PN WO200073788-A1.
XX 07-DEC-2000.
PD 30-MAY-2000; 2000WO-CA00638.
PF 01-JUN-1999; 99US-0137025.
PR (MERI ) MERCK FROSST CANADA & CO.
PA Ng G, O'Neil G;
PI WPI; 2001-049959/06.
DR N-PSDB; AAC91906.
XX Use of gabapentin, 1-(aminomethyl)cyclohexanecarboxylic acid, in assays for
PT identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists
XX Claim 2; Fig 3; 85pp; English.
XX The present invention relates to a method for determining whether a
CC substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a
CC potential agonist or antagonist of the GABA-B receptor. The method
CC comprises exposing cells to 1-(aminomethyl)cyclohexanecarboxylic acid
CC (gabapentin) in the presence or absence of the substance under
CC investigation. The present sequence is human HG20, which was used in the
CC present invention to construct a functional GABA-B receptor, for use in
CC the method of the present invention.
XX Sequence 941 AA;
QY 155 LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKRLLPGYTLLELVNTDQCPCGVGVDRF 214
Db 58 imglmlptkevaksigrvlpavelaleqirnesllrpyfldrlrlydtecdnakglkaf 117
QY 215 FHAIYQTPSTRMVMMLGSGACSEYTESLAKVVPYNNIVQVSGFSTSPALSDRRREPFYFRT 274
Db 118 ydaikygnp--hlmgvggpcsvtsiaeslqgnwlvqlsfaattpvladkkykpyffrt 175
QY 275 VAPDSHNPARIATFRKFGWGTVTTSQNEEVHSLAVNNLVTELEAANISCAATITFA-- 332
Db 176 vpsdnavnpaillklkhgwkrgvtltqdvrfsevrndltgvygedleisdstesfnd 235
QY 333 -ATDFKEQLLLRETDRIIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
Db 236 pctsvek--lkgndvriilqgfdqnnmaakvfccayeenmygkyqwiipwyepswwe 291
QY 392 DQRT-----ACSNHELQLAIVENLIVVSTHNSIVGNVSYSLNNHMFNSQLRKQSAQFHG 446
Db 292 qvhteanssrrclrknl laamegyi-----gvdfeplesskqiktsgktqpqyer 340
QY 447 Q-DGFGSGYGPRIATAATQSDSRRRRRRVGVGTSGHLFPPEAISQYAPQYDAVWAIALA 505
Db 341 eynnkrgvgp-----skfhgyaydgivwiakt 368
QY 506 LRAAEHWRNREEQSKLDGFDYTRSDMAWEFLQMGKHLHFLGSGVPVSFSGPDRVGTAF 565
Db 369 lgramethlhasrhqridqfnydhtlgrilnamnetnffgtgvvfrngermgtikf 428
QY 566 YQIQRGLEPVALYYPATDALDFRCPRCPVKWHSQGVPTAKRVEKLRVATIAPLAFYTI 625
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Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;	
QY 155	LLGLFELSTSRGPRDGLSELGAATMAVEHINRKRLLPGYTLLEVTNDTCQDPGVGVDRF 214
Db 58	imglmpitkevaksigrvlpavelaieqrnesllrpyfldrlrlytecndakglkaf 117
QY 215	FHAIYTOPSRWMLLSGACSEVTESLAKVVPYWNIVQVSGTSPPALSDREFFPYFRT 274
Db 118	ydaikygn--hlmvfgvcpvstlaeslqgnlvqlsfaattpvladkkykpyffrt 175
QY 275	VAPDSSHNPARIAFRKFGWGTVTTFSENEEVLAVNLVTELEAANISCAATITEA-- 332
Db 176	vpsdnavnpaillkilykwrvlgtqdvrfsevrndltgvygedleisdesfsnd 235
QY 333	-ATDFKEQLLLRTRRIIISGSQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
Db 236	pctsvkk---lkgndvriilqgdqmaakvfccayeennvyskyqwiipwyepswwe 291
QY 392	DQRT-----ACSNHELQLAVENTLIVVSTHNSIVGNVNSYSGLNHMFNSQLRKQSAQPHG 446
Db 292	qvhteanssrlrknlllaamegyi-----gvdfeplsskqiktisgktpqgyer 340
QY 447	Q-DGFGSGYGPRIISAATQSDSRRRRRGVVGTSGLHFPPEAISQYAPQYDAVNAIALA 505
Db 341	eynkrsgvvp-----skfhgaydgviwvakt 368
QY 506	LRAAEHRRNEQSKLDGFDYTRSDMAWEFLQMGKHLFGVSGVPFSGPDVRGTTAF 565
Db 369	lqramethassrhqrgdnytdhtlgrilnamnetnffgtvgvfrngermgtikf 428
QY 566	YQIQGGLLEVALYYPATDALDFRCPRCPRWKHSQQVPIAKRVFKLRVATIAPLAFYI 625
Db 429	tqfqsrevkveynavadtleiind---tfrfgseppkdtiileqrkislphysil 485
QY 626	ATLSSVGIALAITLAFLNHLRKLKAIKLSPPKLSNITAVGICFYATVILLGLDHSITLP 685
Db 486	salcilgmimasafifniknrgnklikmsspymanlilggmlsyasiflfgdgsfv- 544
QY 686	SAEDSFATVCTARVYLLSAGSLAFSGMFATYRVRHRTFRGVSFKDKMLQDIOILILV 745
Db 545	-sektfctctvrtwiltgyttafgamfaktwrhaifknv--kmkklidqkliv 601
QY 746	GGLLLVALLVTLWVTPDMEHNLNLETASDRSVYQVQVEVCRSQHTQTLWSLVLY 805
Db 602	ggmliidcilicwqavdprrtvekysmepdpagdisirpllehcenthmtiwigiv 661
QY 806	AYKGLLLVGVYMAWEHRVHKIPALNDSQYICGVSVYVITSAIVVVLNANLISERTLAF 865
Db 662	aygillmlfgclawetrvnsipalndskyigmsvynvgimcilgaavsfldrqpnvqf 721
QY 866	ITIPALITSTATLCLLFIPLKLDIWARNDIIDPVIHSMGLKMECNTRRFVVDRLRLEQ 925
Db 722	civalvifcsticlvfpkl-----itlrtpdaatqnrrfq 761
QY 926	YRVEQNVYKKEQALDAEIKRLERLESGLTTTSTTT--SSSTSLRG----GGLHLP 979
Db 762	f---tqnq--kk-----edsktsvtsvncqastsrleglqsenhrlcm 800
QY 980	ELT-----VTSGISOTPAASK-----NRTPSISG---ILPNLLIS 1011
Db 801	kitekldeventqlqdtpekttyikqnyhqelndilnlnfttestdggkailknhl-- 858
QY 1012	VLPPVIPRASWPSAE 1026
Db 859	---dnpqlqwnntte 870
RESULT 7	
AAW90938	
ID	AAW90938 standard; Protein; 941 AA.
XX	
AC	AAW90938;
XX	

DT XX	14-JUL-2000 (first entry)
DE XX	Human GABA-B receptor protein.
KW KW	GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor; human disease marker; gene therapy; central nervous system; epilepsy; stroke; psychological disease; stress; manic depression; schizophrenia; migraine.
KW KW	
OS XX	Homo sapiens.
XX XX	WO200015786-A1.
PN XX	23-MAR-2000.
PD XX	11-SEP-1999; 99WO-EP06742.
PF XX	14-SEP-1998; 98DE-1041941.
PR XX	04-DEC-1998; 98DE-1056066.
XX XX	(BADI) BASF-LYNX BIOSCIENCE AG.
PI XX	Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;
XX XX	WPI; 2000-283281/24.
DR XX	N-PSDB; AAAL1696.
XX XX	A novel metabotropic receptor complex from the central nervous system, related coding sequences and methods of identifying binding substances, ligands and interactions with other proteins
PT PT	
XX XX	Claim 5; Page 53-56; 66pp; German.
XX XX	This invention describes a novel protein heteromer, containing at least a GABA-B receptor protein and at least a protein (A) or a sequence which has a substitution, inversion, insertion or deletion of one or more amino acid residues and which retains the biological activity of the protein heteromer and which has neuroprotective activity. The encoding nucleic acid (I), the construct, (A) or the protein heteromer are useful for identifying proteins (or nucleic acids encoding such proteins) that show specific binding affinity to (A) or the protein heteromer. The two-hybrid system or biochemical methods can be used to identify interaction domains of metabotropic receptors and use for pharmacotherapeutic intervention. Structural information from the protein or protein complex is useful for identifying and manufacture of substances which have specific binding activity to the protein or protein complex. The protein heteromer and (A), or fragments of these are useful as antigens to generate specific mono- or polyclonal antibodies. (I) is useful for identifying and isolating homologous sequences, as a marker for human disease and for gene therapy. The methods can be used to identify substances, which bind to (A) or (I) and that cause inhibition or activation of functional effects of the GABAergic signal messages in neurons of the central nervous system. The method can also identify substances that inhibit or amplify interactions of (A) with other metabotropic receptors or interaction of ligands with the protein heteromer or (A) or interactions of (A) with G-proteins or other signal transduction molecules. The analysis of the interactions of (A) and GABA-B receptors is important for identifying potential active substances against diseases such as epilepsy, stroke and psychological diseases such as stress, manic depression, schizophrenia, migraine and others. This sequence represents the human GABA-B receptor described in the invention.
XX XX	Sequence 941 AA;

Query Match 15.9%; Score 1066.5; DB 21; Length 941;	
Best Local Similarity 29.5%; Pred. No. 1.3e-85;	
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;	
QY 155	LLGLFELSTSRGPRDGLSELGAATMAVEHINRKRLLPGYTLLEVTNDTCQDPGVGVDRF 214
Db 58	imglmpitkevaksigrvlpavelaieqrnesllrpyfldrlrlytecndakglkaf 117

PT New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor,
 PT useful for identification of (ant)agonists and for treatment of
 PT neurological disorders
 PS Claim 11; Page 29-31; 67pp; English.
 XX
 CC The present sequence is rat gb2 GABA B receptor subunit. Rat gb2
 CC (Rb2) shares sequence homology with rat GABA B receptor rbg1,
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate
 CC receptors. It can be produced in host cells by transforming them with
 CC recombinant expression vector comprising rbg2 encoding cDNA. The cells
 CC that express the receptor are used in the development of drugs for
 CC treatment of neurological and psychiatric disorders, for pharmacological,
 CC physiological, functional, or other investigational analysis of
 CC gb2 GABA B receptor, its agonists or antagonists and for determining the
 CC ability of a chemical to bind to a mammalian gb2 GABA B receptor in
 CC vitro. They may also be used for the preparation of antibodies to rbg2
 CC which can be used in diagnostic assays.
 XX
 SQ Sequence 940 AA;

Query Match 16.0%; Score 1069.5; DB 21; Length 940;
 Best Local Similarity 29.6%; Pred. No. 7e-86;
 Matches 271; Conservative 159; Mismatches 340; Indels 145; Gaps 20;

Qy 155 LGLFELSTSRGPRDGLSELGAATMAVEHINRKRLLPGTYLELVTNDQCPGVGVDRF 214
 Db 57 imglmlptkevaksgisrgvlpavellaieqirnesllrpyfldrlrydtecdnakglakf 116
 Qy 215 FHAIYQSTRMVMLLGSCEVTESLAKVVPYWNIVQVSFGSTSPALSDRRFPFYPT 274
 Db 117 ydaikygnp--hlmvfggvcpsvtsiaeslqgnvlgvlsfaattpvladckkyfyfrt 174
 Qy 275 VAPDSHNPARTAFIRKFGWGVTVTPSQNEEVHSLAVNNLVTELEAANISCAATITFA-- 332
 Db 175 vpsdnvapailkllkhfrwrvgtltqdxgrfsevrndltgvygedieisdesfnd 234
 Qy 333 -ATDFKEQLLLRETRDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
 Db 235 pctsylvk----lkgndvrlilqfgdnpmaakvfccafeesmfqskqywiipgyepawwe 290
 Qy 392 D-----QRTACSNHELOLAVENLIVVVTNSIVGNVVSGLNNHMFNSOLRKQSAQPHG 446
 Db 291 qvhveansrcrlrrsllaamegyi-----gvdfepalskqiktisgktpqqr 339
 Qy 447 Q-DGFGSGVGPRIATAATQSDSRRRRRRGVGTSGGHLFPEATISOYAPQTYDAVWATA 505
 Db 340 eynskrsgvpp-----skfhgaydgilwviakt 367
 Qy 506 LRAAEHRNRNEQSKLDGDFYTRSDMAWEFLQMQKGLHFLGVSGVPVFSFGPDRVGTAF 565
 Db 368 lgrametihassrhqirqfnydhtlgtkiiilnametnffvgvqvfngermgtikf 427
 Qy 566 YQIQGGLLEPVALYPTADLDFRCPRPVKWSQVPIAKRVFKLRVATAPLAPYTI 625
 Db 428 tqfgdsrevkqgeynavadtileind--tirfggseppkdtileqlrkisiplysil 484
 Qy 626 ATLSVSGIALATFLAFNLHFRKLAIKLSSPKLSNITAVGCIFFVATVILLGLDHSFLP 685
 Db 485 saltlilmmasafiffnknnrqkllkmsppmnnlilgmslyasiflfdgsfv- 543
 Qy 686 SAEDSFATVCTARVYLLSAGFSLAFSGFMAKYRVHRIFRTGVSFKDKMLQIDILLY 745
 Db 544 -sektfelctvrtwiltvygtafamfakturvhafknv--knkklkdkqkllviv 600
 Qy 746 GGLLVLDALLVTLVWVTPDMERHLNHLTLEISATDSVVYQVQVEVCRSOHTQTWLSVLY 805
 Db 601 ggmllidicilicwqavdprrrtverysmepdpagdisirpillehcenthmtiwigiv 660
 Qy 806 AYKGLLLVGVYVMANETRVKIPALNDSQYIGVSYSVVTSAIVVVLANLISERVTLAF 865
 Db 661 aykglilmfqcfawetrvnsipalndskygmsvynvglmciigaavsfiltrdqpnvqf 720

Qy 866 ITITALILTSTATLCLLFIPLKHLDIWANDIIDPVIHSMGLKMECNTRRFVVDREIQ 925
 Db 721 civalviifcsticlvfvpkl-----itlrtpdaatqrrfq 760
 Qy 926 YRVEQNVRYKKEIQALDAEIRKLERLESGLTSTTT--SSSTSLLTG---GGHLKP 979
 Db 761 f---tqnq--kk-----edsktstsvtnqastsrleglsenhrilm 799
 Qy 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011
 Db 800 kiteidkdlleetvmlqtdtpekttyikqhqyelndilslnftestdgkalknhl-- 857
 Qy 1012 VLPPVIPRASWPSAE 1026
 Db 858 ---dqnpqlqwnnte 869

RESULT 6
 AAY29796 standard; Protein; 941 AA.
 XX
 AC AAY29796;
 DT 15-NOV-1999 (first entry)
 XX
 DE Human gamma-amino-butyric acid B receptor subunit HG20.
 KW Gamma-amino-butyric acid B receptor subunit; HG20; GABABRIA;
 KW depression; epilepsy; neuropsychiatric disorder; dementia;
 KW muscular contraction; central nervous system disorder.
 OS Homo sapiens.
 XX
 PN WO9940114-AL.
 PD 12-AUG-1999.
 XX
 PF 03-FEB-1999; 99WO-US02361.
 XX
 PR 05-FEB-1998; 98US-0073767.
 XX
 PA (MERI) MERCK & CO INC.
 PA (MERI) MERCK FROSST CANADA INC.
 PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
 PA (USSH) US NAT INST OF HEALTH.
 XX
 PI Bonner TI, Bonner TP, Clark J, Kolakowski LF, Liu Q;
 PI McDonald T, Ng GYK;
 XX
 DR WPL; 1999-527300/44.
 DR N-PSDB; AAZ06968.
 XX
 PT New DNA encoding human and murine receptor subunits, useful for
 PT identifying agonists and antagonists for treatment of depression,
 PT epilepsy and neuropsychiatric disorders
 XX
 PS Claim 7; Fig 2; 128pp; English.
 XX
 CC The present sequence represents a human gamma-amino-butyric acid (GABA)
 CC B receptor (GABAB) subunit designated HG20. The present invention
 CC also describes the GABAB subunit designated GABABRIA. Cells expressing
 CC the new receptor subunits are useful for identifying GABAB agonists
 CC and antagonists. HG20 proteins and their antagonists are useful for
 CC inhibiting HG20 or GABAB function, useful for treating depression,
 CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
 CC and central nervous system disorders.
 XX
 SQ Sequence 941 AA;

Query Match 15.9%; Score 1066.5; DB 20; Length 941;
 Best Local Similarity 29.5%; Pred. No. 1.3e-85;

CC useful for treating drug addiction. Antagonists are used to treat
CC Alzheimer's disease. Functional assays were not possible with GABAB1
CC alone, so identification of a new GABAB2 polypeptide is useful for high
CC throughput screening assays for agonists or antagonists against GABAB
CC receptors using co-expression of GABAB1/R2. The pharmacological and
CC signal transduction properties of the two receptors GABAB1 and R2 match
CC those of native GABAB receptors in the brain.
XX
SQ Sequence 898 AA;

Query Match 16.0%; Score 1071.5; DB 20; Length 898;
Best Local Similarity 29.5%; Pred No. 4.3e-86;
Matches 271; Conservative 161; Mismatches 342; Indels 145; Gaps 20;

Qy 151 GKVLGLFELSTSGRPDGLSELGAATMAVEHNRKLLPGYTLBELVTNDTQCDPGVG 210
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 11 gplsmgmlptkavkgsigrvlpavelaieqirnesllrpyfidrlrlydtecdnag 70
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 211 VDRFFHAIYQSTRMVLGSAESVETSLAKVWPVWNIQVSPGSTPALSDRRPEPY 270
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 71 lkafydaikygnp--hlmgfvgvcpvstsliaeslqgnlvqlsfaatpvladkkypy 128
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 271 FVRTVADSSHNPARIAFTRKFGWGVTTFQNEEVHSLAVNNLVTELEAANISCAATIT 330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 129 firtvpsdnvnapalkllkhyqkrvgtltqgvrfsevrnditgvlgyedieisotes 188
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 331 FA---ATDFKEQLLLRETDTRIIIGSFQELAPQICELAYRLRMFCGADYAWILHESMGA 387
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 189 fsndpctsvkk---lkgndvriilqgfdqpnmaakvfccayeenmygskygwiipgyep 244
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 388 PWWPQRT-----ACSNHEQLQAVENLIVVTHNSIVGNVSYGLNHNMFNSOLRQKSA 442
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 245 sweqvhteanssrclrkllaamegyi-----gvdfep1sskqiktisgktpq 293
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 443 QFHGQ-DGFGSGYGRISTAAATQSDSRRRRRGVGTSGHLPPEALISOYAPQTYDAVWA 501
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 294 qyereynkrsgvvp-----skfhgyaydgilw 321
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 502 IALALRAAEHWRNRNEQSKLDGFDYTRSDMAWEFTQMGKHLFLGVSGVPVSFGPDVRG 561
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 322 iaktlgramethasrhqrigdfnydhtlgrilnamnetnffgvtgqvfvfngermg 381
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 562 TTAFYQIQGLLEPVALYYPATDALDFRCPRCPVWHSQVPIAKRVKLRVATIAPLA 621
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 382 tikftfgdsvrevkgeynavadtieind---tirfgseppkdktilleqirkislp1 438
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 622 FYTIATLSSVGLATLAFNLHPRKKAIAKLSSPKLSNITAVGCFIVYATVILLGLDH 681
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 439 ysilisaltlilgmimasafiffiknrnqkikmsspymnnlililgmlsyasiflfgldg 498
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 682 STLPSAEDSFATVCTARVVLVLSAGSLAFSGMFAKTYRVHRTFTGVSFKDKMLQDIQL 741
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 499 sfv--sektfelctvrtwiltvgtaytafamfaktwvhaifknv--kmkxiikdql 554
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 742 ILLVGLLLVDALLVTLVWVTPDMERHLNLTLEISATRSVVYQVQVEVCRSQHTQTWL 801
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 555 lviivgmlilidicilicqavqplrttekysemepagardisirplehcenthmtiwl 614
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 802 SVLYAYKGLLVGVYMAWETHVKIPALNDQYIGVSVYVITSVAVVVLNANLISERV 861
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 615 givvaykgllmifgflawetwnvsiipalndskysgmvsynvgimciigaavsfiltrdqp 674
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 862 TLAFITITALTITATLCLLFIPLKLDIWARNDIIDPVIHSMGLKMECNTRRFVVD 921
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 675 nvqfcivalvifcestilclvfpkl-----itlrtpdaatqn 714
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 922 RELQYRVQNVRYKKEIQALDAEIRKLERLESGLTITTTSTTT---SSSTSLTGG---GG 975
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 715 rrfqf---tqnq--kk-----edsktstsvtsvngqasterleglsenh 753
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 976 HLKPELT-----VTGSISOTPAASK-----NRTPSISG---ILPN 1007
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Db 754 rlrmkiteldkleevtmqldtpekttyikqhyqelndilnlnftestdggkailkn 813
Qy 1008 LLLSVLPVPIPRASWPSAE 1026
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 814 hl-----dgnpqlqwnnte 827
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
RESULT 4
AA70326 AAY70326 standard; Protein; 898 AA.
XX AC AAY70326;
XX DT 21-JUN-2000 (first entry)
XX DE Human gamma amino butyric acid receptor, GABA-B-R2 protein.
XX KW Gamma amino butyric acid; GABA-B-R2; human; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antispasmodic; antidiarrhetic;
KW uterine; analgesic; antitussive; agonist; neuroprotective; nootropic;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 438..461
FT FT /label= Transmembrane_domain-I
FT Domain 475..501
FT FT /label= Transmembrane_domain-II
FT Domain 513..535
FT FT /label= Transmembrane_domain-III
FT Domain 554..576
FT FT /label= Transmembrane_domain-IV
FT Domain 612..634
FT FT /label= Transmembrane_domain-V
FT Domain 648..670
FT FT /label= Transmembrane_domain-VI
FT Domain 676..701
FT FT /label= Transmembrane_domain-VII
XX WO200012692-A1.
XX PD 09-MAR-2000.
XX PF 27-AUG-1999; 99WO-US19651.
XX PR 27-AUG-1998; 98US-0141760.
PR 16-OCT-1998; 98WO-US22033.
PR 04-NOV-1998; 98US-0186664.
PR 15-DEC-1998; 98US-0211755.
XX PA (SYNA-) SYNAPTIC PHARM CORP.
XX PI Jones KA, Laz TM, Borowsky B;
XX WPI; 2000-246751/21.
DR N-PSDB; AAZ51399.
XX PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
PT detecting receptor agonists useful for treating e.g. asthma,
PT incontinence, and Alzheimer's disease.
XX PS Claim 9; Fig 5; 260pp; English.
XX CC The present amino acid sequence is the human GABA (gamma amino butyric
CC acid)-B-R2 receptor protein isolated from human hippocampus cDNA library.
CC The coding region of GABA-B-R2 is cloned into the expression vector
CC pEXJ-HRT37 and the plasmid is designated as TL-267 (ATCC No. 203515).
CC GABA-B is a major inhibitory neurotransmitter, the receptors of which
CC are widely distributed throughout the central nervous system. GABA-B-R2
CC receptor has anticonvulsant, antispasmodic, uterine, analgesic,
CC antitussive, antidiarrhetic, nootropic and neuroprotective activity.


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XX PS Claim 2; Page 51-59; 62pp; German.
XX CC This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor
CC which is described in the method of the invention.
XX SQ Sequence 1305 AA;

Query Match 100.0%; Score 6705; DB 22; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIIPVQGTGRYPMPAVGLRLVLALAWATSAAMMESSAELQALGHEAIRPGAASISTS 60
Db 1 mriipvqgtrypmpavglrlvlalawatsaaamessaelqalghaeairpgaasists 60
Qy 61 SPSSPPGESASTVTAGTPPIPRSDWKYKRTVKRRQRLNHSNLPGSTNASHAHLL 120
Db 61 spssppgesastvtagtpiprdsdkyrtvkrrqrlnshsnlpgstnashahll 120
Qy 121 NLPQRQYLKVNQVFERSESRMSPAEQRNHGKTVLGLFELSTSRGPRPDGLSELGAATM 180
Db 121 nlpqrqylkvnqvferseermspaemqrnhgkivlglfelstrgprpdglseigaatm 180
Qy 181 AVEHINRKLRLPGYTLELVNTDTCQDPGVDRFFHAIYTPQSTRMVMLLGSACSEVTES 240
Db 181 avehinrklrlpgytlevntdtdcpvgvdrffhaiytpqstrmvmllgsacsevt 240
Qy 241 LAKVVPYNIVQVSGSTSPALSDRREFPYFYRTVAPDSSHNPARIATIRKFGWGVTTTF 300
Db 241 lakvvpynivqvsfstpsaldrrefpyfyrvtapdsshnpariatirfkfgwgttf 300
Qy 301 SONEVHSLAVNNLVELEAANISCAATTFEATDFKEQLLLRETDTRIIGSFSOELA 360
Db 301 sneevhslavnnlveleaaniscaatitfaatdfkeqlllretdtriiigsfsqela 360
Qy 361 PQILCEAYRLRMFGADYAWILHESMGAPWMPDQRTACSNHELQALAVENLIVVSTHNSIVG 420
Db 361 pqilceayrlrmfgadyawilhesmgapwmpdqrtacsnhelqlavenlivvsthnsivg 420
Qy 421 NNVSYSGLNNHMFNSQLRKQSQAFHGQDGGSGYGRPRISATATQSDSRRRRRRGVVGTSG 480
Db 421 nnvsyyslennhmfnsqrlrkqsafhgqdgsgygrprisiaatqsdrrrrrgvvgts 480
Qy 481 GHLPFPALISOYAPQTYDAWATLALRAAEHWRNEEQSKLDGFDYTRSDMAWEFLQOM 540
Db 481 ghlpfpalsyapqtydawaalalraaeenrneeekldgfdytrsdmaweflqqm 540
Qy 541 GKLHFLGVSGPVFSFGSDRVGTTAFYQIQRGLEPEVALYPAFDALDFRCPRCPVKWHS 600
Db 541 gklhflgvsgpvfsfgsdrvgttafyqiqrglepevalypatdaldfrpcrcpvkwhs 600
Qy 601 GOVPKAKRVFKLRVATIAPLAFYTTIATLSSVGIATAITFLAFNLHFRKLAIKLSSPKLS 660
Db 601 gvvpkavrkvfklrvatiaplafyttiattlssvgiataitflafnlhfrkllaiklsspkls 660
Qy 661 NITAVGCCFVYATVILLGLDHTLSAEPSFATVCTARVYLLSAGFSLAGFSMPAKTYRV 720
Db 661 nitavgccfvyatvillglldhtlsaeapsfatvctarvyllsagfslagfsmfaktyrv 720
Qy 721 HRIFRTGVSFKDKMLQDIQLILLVGLLLVDALLVTLVWVTPMERHLNLTLEISATD 780
Db 721 hrifrtgsvfkdkmlqdiqlillvglldvallvltlvwvtpmerhlntlleisatd 780

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```

Qy 781 RSVYVQVEVCRSQHTOTWLSVLYAYKGLLLVGVYMAWETRHVKIPALNDSQXIGVSV 840
Db 781 rsvyvpqvevcrsqhtqtwlsvlyaykglilvvgymawetrhvkipalndsxyigvsv 840
Qy 841 YSVWITSIVVVLANLISERVTLAFITITALITSTATFLCLLFPKLDHIWARNDIIDP 900
Db 841 ysvwitsivvvlanliservtlaftitalitsttatlcllfpkldhiwarndiidp 900
Qy 901 VIHSMGLKMECNTRFRVDDRELQYRVQNRVYKKEIQALDAEIRKLERLLESLTWT 960
Db 901 vihsmglkmecontrfrvddrelqyrvvqnrvykkelqaldaeirklerllesglttt 960
Qy 961 STTSSSTSLTGGHKLPELTVTSGISQTPAASKNRTPSISGILPNLLSVLPVIPA 1020
Db 961 sttssstslttggghklpeltvtsgisqtpaasknrtpsissgilpnllsvlpvipra 1020
Qy 1021 SWPAAEYMQIPMRRSVTFASQPOLBEACLPADQLINLRLAHQQAETAGTLNRLRGIFS 1080
Db 1021 swpaeymqipmrsvtfsaqpolbeaclpaqdlinlrlahqgateaktglinrlrgifs 1080
Qy 1081 RTTSNKGSTASLADOKGLKAAFKSHMGLFTRLIPSSQTASCAINYNPNQDSIPSEASS 1140
Db 1081 rttssnkgstasladoqglkaafkshmgfltrlipssqtascnainynpnqdsipseass 1140
Qy 1141 HPNGNHLKPIHRGSLTKSGTHLDHLTKDPNPLPIPTISGGEQDQTLGCKYVKLLTKVN 1200
Db 1141 hpngnhlkipihrgsltksgthldhltkdpnflpriptisgggedqdtlgckyyklltkvn 1200
Qy 1201 FOLPSNRPSVVQPPSLRERVRGSPRPHRLIPTPTCSLSALAESEDRPDGDSITLGSCK 1260
Db 1201 folpsnrpsvvqppslrervrgrsprphrlipptcsalsalaeasedrpgdstslgsck 1260
Qy 1261 SIPRISLQVTSGGTGWKSMETVGRSLSLGDSQEEQQAPANGTE 1305
Db 1261 siprslqvtsggtgwksmetvgksrslsgdsqeeqqapangte 1305

RESULT 2
AAB86160
ID AAB86160 standard; Protein; 1220 AA.
XX AAB86160;
AC AAB86160;
XX 03-AUG-2001 (first entry)
DT 03-AUG-2001 (first entry)
DE D. melanogaster GABA-B receptor protein SEQ ID 4.
XX GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
XX insecticide; transgenic invertebrate; plant protection agent;
XX human medicine; veterinary medicine; insect.
XX Drosophila melanogaster.
XX DEL9955408-AI.
XX 23-MAY-2001.
XX 18-NOV-1999; 99DE-1055408.
XX 18-NOV-1999; 99DE-1055408.
XX (FARB ) BAYER AG.
XX Raming K, Mezler M, Mueller T;
XX WPI; 2001-318282/34.
XX N-PSDB; AAH20520.
XX New invertebrate gamma-aminobutyric acid receptor proteins, useful in
XX screening for potential insecticides, for plant protection or medicine,
XX also related nucleic acid
XX Claim 2; Page 32-39; 62pp; German.

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:00:32 ; Search time 52.81 Seconds
(without alignments)
1830.442 Million cell updates/sec

Title: US-09-715-962-6

Perfect score: 6705

Sequence: 1 MRIIPVQCTRYGPMPAVGL.....RLSLGDSQEEQQAPANGTE 1305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
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6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
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11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID58/gcgdata/geneseq/geneseq/AA1991.DAT.*
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20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6705	100.0	1305	22 AAB86161	D. melanogaster GA
2	1229	18.3	1220	22 AAB86160	D. melanogaster GA
3	1071.5	16.0	898	20 AAY14082	Human GABABR2 prot
4	1071.5	16.0	898	21 AAY70326	Human gamma amino
5	1069.5	16.0	940	21 AAY44343	Rat gb2 GABA B rec
6	1066.5	15.9	941	20 AAY29796	Human gamma-amino-
7	1066.5	15.9	941	21 AAW90938	Human GABA-B recep
8	1066.5	15.9	941	21 AAY51928	Human GABA-B recep
9	1066.5	15.9	941	21 AAY70328	Human GABA-B-R2 re
10	1066.5	15.9	941	21 AAY79202	Human GABAB recept
11	1066.5	15.9	941	21 AAY44342	Human gb2 GABA B r

12	1066.5	15.9	941	22 AAB50088	HG20 protein seque
13	1066.5	15.9	943	20 AAY28837	Human GABABR2 rece
14	1065.5	15.9	940	21 AAW90937	Rat GABA-B recepto
15	1065.5	15.9	940	21 AAY70327	Rat gamma amino bu
16	1065.5	15.9	1303	20 AAY49132	GABA-BR2*Gqo5 fusi
17	1064.5	15.9	940	21 AAY51927	Rat GABA-B recepto
18	1058.5	15.8	883	20 AAY14081	Rat GABABR2 protei
19	1058.5	15.8	941	21 AAY68743	A human gamma-amin
20	1058	15.7	914	21 AAY44344	Protein-1 related
21	1055	15.7	965	21 AAY44345	Protein-2 related
22	1018.5	15.2	840	22 AAB86159	D. melanogaster GA
23	994	14.8	844	19 AAW40118	Rat GABA-BR1b rece
24	994	14.8	844	19 AAW40119	Human GABA-BR1b re
25	994	14.8	844	20 AAY28839	Human GABABR1b rec
26	994	14.8	844	20 AAY14102	Human GABAB recept
27	994	14.8	844	21 AAY32467	Human G-protein co
28	992.5	14.8	960	19 AAW40116	Rat GABA-BR1a rece
29	992.5	14.8	961	20 AAY29798	Human gamma-amino-
30	992	14.8	844	20 AAY28842	Rat GABABR1b rece
31	992	14.8	844	20 AAY49123	Rat GABABR1b prote
32	991.5	14.8	960	21 AAY83145	Human GABABIAA rec
33	991.5	14.8	961	20 AAY28838	Human GABABIAA rec
34	991.5	14.8	961	20 AAY14101	Human GABAB recept
35	991.5	14.8	1323	20 AAY49133	GABA-BR1a*Gqo5 fus
36	990.5	14.8	960	20 AAY28841	Human GABABIAA rec
37	990.5	14.8	960	20 AAY49122	Rat GABABR1a rece
38	989.5	14.8	960	20 AAY29797	Rat GABABR1a prote
39	988.5	14.7	899	20 AAY14107	Murine gamma-amino
40	987.5	14.7	960	22 AAB50089	Human GABAB recept
41	984	14.7	892	20 AAY14109	Murine GABA-B-R1a.
42	982	14.6	962	22 AAB50090	Human GABAB recept
43	979.5	14.6	793	19 AAW40117	Human GABA-B-R1a.
44	976	14.6	859	20 AAY34111	Human GABA recepto
45	976	14.6	859	20 AAY30311	Amino acid sequenc

ALIGNMENTS

RESULT 1
ID AAB86161 standard; Protein; 1305 AA.
AC AAB86161;
DT 03-AUG-2001 (first entry)
XX D. melanogaster GABA-B receptor protein SEQ ID 6.
DE GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect.
XX Drosophila melanogaster.
OS DE19955408-A1.
PN 23-MAY-2001.
XX 18-NOV-1999; 99DE-1055408.
PF 18-NOV-1999; 99DE-1055408.
XX 18-NOV-1999; 99DE-1055408.
PR (FARB) BAYER AG.
XX Raming K, Mezler M, Mueller T;
XX WPI; 2001-318282/34.
XX N-PSDB; AAH20521.
XX New invertebrate gamma-aminobutyric acid receptor proteins, useful in
PT screening for potential insecticides, for plant protection or medicine,
PT also related nucleic acid

Db 258 RPGEFEKIIKRLLETPNARAVIMFANEDDIRILEAAKLNQSG-HFLWIGSDSWGSKIA 316
QY 388 PWPDPQRTACSNHELQLAIVENLIWSTHNSIVGNVSYGLNNH-----MENSOLRKQSA 442
Db 317 PVTQOEIEA-----EGAV-----TILPKRASIDGFDYFRSRTLANNRRNYWEFA 360
QY 443 QFHGQDGF-----SGYQPRISIAATQSDSRRRRRGGVGTSGGHLFPEAISQYAPQTYDAV 499
Db 361 EF-WEENFGCKLGHSHKRNHIKCTGLERIADSSYEQEGKVQF-----VIDAV 409
QY 500 WAIALALRAAAEHRNE-----EQSKLDGFDYTRSDMAWEFLQOMGKLHFLGVS 549
Db 410 YSMAYAL-----HNMKDLCPGYIGLCPRMSTIDG-----KELLGYIRAVNENGSA 455
QY 550 G-PVSFS-GPDRVGTTFATQIQ-----RGLLEPVAL 578
Db 456 GTPVTFNENGADPGRYDIFQYQITNKSTKEYKVIGHWTNQLHLKVEDMQWAHREHTHPASV 515
QY 579 -----YYPATDALDFRCPRC-----RP----- 595
Db 516 CSLPCPKGERKKTIVKGPCWCHCERCEGYNVQDELS--CELCPDQDRPNNRTGCQIIP 573
QY 596 ----VKWHS--GOVPIAKRVFKLVAITAPLAFVTIATFLSSVGIALAITFLAFNLHFRKLK 650
Db 574 IIKLEHSPWAVPVFVAILGIITTF-----VIVTFVRYN-----DTP 612
QY 651 AIKLSPKLSNTAVGICFYAVAVIILGLDHLTPSAEDSFATVCTARVYLLSAGFSLAF 710
Db 613 IVRASGRELSYVLLGTGFLCYSTFL-----MIAAPDTI--ICSPRRVFLGLGMCFSY 663
QY 711 GSMFAKTYRVHRIETR-TGSVFKDKMLQDLOLILLVGGLLLDALLVTLWVTD----- 764
Db 664 AALLTKNRIHRIFEQKKSVTAPKFI SPASQLVITFSLISVQLLGVFVWVVDPPHIII 723
QY 765 -----MERHLNHLTLEISATDRSVVYQPVQVEVCRSQTWTLSVLYAYKGLLVVGVY 817
Db 724 DYGEQRTLDPEKARGVLKCDISDLSL-----ICS-----LGYSILLMVTCTV 765
QY 818 MAWETRHVKIPALNDSQYIGSVYSV-VITSIVVVLNLI--SERVTLAFITITALILT 874
Db 766 YANKTRGVP-ETFNEAKPIGFTWTTCTIWLAFIPIFFGTAQSAEKWYIQTTLTIVSMLS 824
QY 875 STATLCLLFIPLKLDIWARNDIIDPVIHSMGLKMECNTRRFVVDRELOQYRVEV----- 930
Db 825 SASVSLGMLYMPKVYII-----IFHP-----EQNVQ-----KKRSEKAVVTAAT 864
QY 931 -QNRVYKKEIQALDAIRKLERLLESGLTSTTTSSTS 969
Db 865 MQSKLIQGNDRPNGEVK--SELCELETNTSSTKTYIS 902

Search completed: April 30, 2002, 10:05:11
Job time: 789 sec

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; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-4

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Query Match	5.18;	Score 339;	DB 4;	Length 867;
Best Local Similarity	19.28;	Pred. No. 3e-21;		
Matches 195;	Conservative 163;	Mismatches 367;	Indels 290;	Gaps 39;
QY 164	SRGP-----RPDGLSELGAATMAVEHINR-KRLLPGGVTL-----	196		
DB 4	AKGSGVPCGDIKRENGHURLEAMLYALQDQNSDPNLLPNVTLGARILDTCSRDTYALEQ 63			
QY 197	-----ELVNTDQCPDGVGDREFFHAIYTOPSTRMVMLLGSACSEVTESLAKVVPY 247			
DB 64	SLTFVQALIQKDTSDVRCTNGE-----PPVFVKPE-KVVGVGASGSSVISIVANILRL 116			
QY 248	WNIYVQVSGSTSPALSDRREPFYFRTVAPDSSHNPARIARIRKGCWGTVTTFSSONEVH 307			
DB 117	FOIPOISYASTAPELSDRRYDTSRVVPPDSFQAQAVDVKALGWMYVLTSLASEGSYG 176			
QY 308	SLAVNNLVTELEAANISCAATITTAATDFKQLL-----LLRETDTRIIGSFSOEL 359			
DB 177	EKGVESFTQISKEAGGLCIAOSVRIPQERKORTIDFDRIIKQLDTPNSRAVVFANDED 236			
QY 360	APQICLAYRLRMFGADYAWILHESMGAPWMPDQRTACSNHELQALAVENLIVVSTHNSIV 419			
DB 237	IKQILAAAKRADQVG-HFLWVGSDSWGSKINP-----LHQHEDIAEGAITIQPKRATV 288			
QY 420	GNNVSYSGLNNHMFNSQLRKSOAFHGODGFGSGVGPRISTAATOSDSRRRRRRCVVGTS 479			
DB 289	-----EGFDAYFTSRITLNNRRNNVWFAEYWEENFNCKLTISGSKEDTDRKCTG----- 337			
QY 480	GGHLFPEAI-----SOYAPQ-----TYDAWATALALRAAAEEHWRN-----EEQSKL 522			
DB 338	-----QERIGKDSNYEQEGKVQFVIDAYVMAHAL-----HHMKNKDLCADYRCVCEMEQA 388			
QY 523	DGEDYTRSDMAWEFLQOMKLIHFLGSG-PSVSFS-GPDVRVGTFATFYQIO----- 569			
DB 389	GG-----KLLKYIRNNVFNFGSAGTPVMFNKNGDAPGRYDIFQYTTNTSPGYRL 439			
QY 570	-----RGL-----LEPVALYYP 582			
DB 440	IGQWTELOLNIEMQMGKGVREIPASVCTLPCKPGQRKKTKQTPGCWTCPCDGYQVQ 499			
QY 583	TDALDFRCPRC-----RPVKWHSG--QVPIAKRFVKRLVATIAPLAFYTIATLSSVGIALA 636			
DB 500	FD--EMTCHQCPYDQRPNNRNTGCQDIPILKEWSPWAVP-----VFLAMLGIAT 550			
QY 637	ITFLAFNLHFRKLKAIKLSSPKLSNITAVGCIFFYATVILILGLDHSITLPSABDSFATVCT 696			
DB 551	IFVMATFIRYNDTPIVRASGRELSVVLITGFLCVIITFLM-----IAKPDVA-VCS 601			
QY 697	ARVYLLSAGFSLAFSGMFAKRVYRHIFTR-TGSVFKOKMLQDIQILILVGLLGLLDALL 755			
DB 602	FRFVFLGMCISYAALLTKNRIYRIEFGKKSVTAPRLISPTSQLAITSSLISVQLLG 661			
QY 756	VTLWVVTDPMERHLNHLFLEISATDRSVVYQDVE--VCRSOHTQWLSVLYAYKGLLV 813			
DB 662	VFIWFGVDP-----PNIIDY---DEHKTMPNQARGVLKCDITDLQITCSLGSYILLW 713			
QY 814	GVVYMAWETRHVKIPALNDSQIGYSVYSV-VITSIAVVVLANLI--SERVTIARITITA 870			
DB 714	TCTVYAIKTRGVF-ENFNEAKPIGFTMYTTCIVLWIAFIPFPGTAQSAEKLYIQTTTLTI 772			
QY 871	LILTSTATLCLLFPKPLHDIWARNDIIDPVIHSMGLKMECNTRFRVDDRRELOVRVEV 930			
DB 773	SMNLSASVALGMLYMPKVYII-----IFHP-----ELNVQK 803			
QY 931	QNRVYKKEIQALDAEIRKLERLLESGLTSTTTSSSTSLTTGGGHKLPELTVTSGISQT 990			
DB 804	KRRSGFAVVTA-----ATMSSRLSHK 824			

QY 991 PAASKN---RTPTSIGILPNLLSVLPVPIRASWPSEAQMIPMRRSVTFASQP 1042
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Db 825 PSDRPNGEAKTELCEVDPN---NCIPPV--RK\$-----YOKSVTWTPIP 864

RESULT 15

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US-08-855-146-2
: Sequence 2, Application US/08855146
: Patent No. 6221609
: GENERAL INFORMATION:
: APPLICANT: Belagaje, Rama M.
: APPLICANT: Wu, Su
: TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
: TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Eli Lilly and Company
: STREET: Lilly Corporate Center/Patent Department
: CITY: Indianapolis
: STATE: IN
: COUNTRY: USA
: ZIP: 46285
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/855,146
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/021,243
: FILING DATE: 07-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Webster, Thomas D.
: REGISTRATION NUMBER: 39,872
: REFERENCE/DOCKET NUMBER: X-10836
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (317) 276-63334
: TELEFAX: (317)276-2764
: INFORMATION FOR SEQ ID NO. 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 908 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-855-146-2

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Query Match 5.0%; Score 336.5; DB 4; Length 908;
Best Local Similarity 20.7%; Pred. No. 5.5e-21;
Matches 207; Conservative 153; Mismatches 339; Indels 301; Gaps 46;

[illegible]

QY 809 GLLLVGVYMAWETRHVKIPA-LNDXOYIGVSVSVVITSATVAVVLANLISERVTLAFIT 867
Db 736 VLLIALCTLYAFKTR--KCPENFNEAKFIGTMYTTCI-----IWLAFLP 778
QY 868 ITALILTST-----TATLCL-----LFIPKLHDI 891
Db 779 I--FVVTSSDYRVQTTMCVSVLSGVSVLGCLFAPKLHII 817

RESULT 13
US-09-258-523-2
; Sequence 2, Application US/09258523
; Patent No. 6103475
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/337,797
; FILING DATE: NO. 6103475ember 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9431
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 872 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-258-523-2

Query Match 5.1%; Score 340.5; DB 3; Length 872;
Best Local Similarity 21.7%; Pred. No. 2.2e-21;
Matches 191; Conservative 113; Mismatches 344; Indels 233; Gaps 35;
QY 151 GKIVLGLFELSTSRGPRD-----GLSELGAATMAVEHINR-KRLLPG----- 193
Db 30 GDLVLGLFPVHKGGAEDCGPVNHRGIQRLLEAMLFALDRINRDPHLLPGVRLGAHIL 89
QY 194 -----TYLELVNTQCDPGVGVDRFH-----AIYQSTRMVMLLGSACSVTE 239
Db 90 DSCSKDTHALEQALDVRASLSRGADGSRHICPDGVSATHGDAPTAITGVIGGSVDSVI 149
QY 240 SLAKVVPYNNVQVSPSPALSDRREFFYFVTVAPDSSHNPARIAFTRKTCGWGTVTT 299
Db 150 QVANLLRLQIPOISYASTSAKLSKSRDYDFARTVPPDFQAKAMAEILRRFNWTVYST 209

QY 300 FSNEEVHSLAVNNLVTELEAANIACAATI-----TFAATDFKEOL-LLLRETDTRIIG 353
Db 210 VASEGDYGETGIEAFELERARNI-CVATSEKVGSRAMRAAFEGVVYRALLQKPSARVAVL 268
QY 354 SFSOELAPQIILCEAYRLRMFGADYAWILHESMGA----- 387
Db 269 FTRSEDARELLAASQRL---NASFTWASDGNWGALESVVAGSEGAEGAITIELASYPTS 325
QY 388 -----PW-----WPDQRTACSNHEHLQLAVERNLIIV- 412
Db 326 DFASYFQSLDPWNNSRNPWFREFW-EORPRCSFRORDCAHSLRAVPFPQESKIMFVVNA 384
QY 413 -----STHNSIVGNVNSYSLNNHMFNSQLRKSQAQFHGODGFGSGYSPRISIAAT 463
Db 385 VYMAHALHNNHRLALCPNTRCLDAMRPVNGRRLYK---DFVLNVKFDAPFRP----ADT 437
QY 464 OSDSRRRRRGVGTSGGHLFPEAISQVAPQYDAVMAIALALRAAEHHRNEEQSKLD 523
Db 438 HNEVFDR-----FGDGIGRYNIFTY-----LRAGSGRYRYQKVGYNAE 476
QY 524 GFDTYTRSDMAWEFLQOMGKLHFLGVSGPVFSFG-----PDRVGTGTAFYQIQRGLLEPVA 577
Db 477 GLTLDTSLIPWASPS-----AGPLPASRCSEPCLONEVKSVQPGVCCWLCIPCO 526
QY 578 LYYPATDALDFRCPRCPVKH-----SGQVPIAKRVFKLRVA-TIAPLAFYTIATLSSVG 632
Db 527 PYEYRLD--EFTCADCGLYWPNASLTGCFELPOEYIRMGDAWAGPV---TIACLG--- 578
QY 633 IALAITF-LAFNLHFRKLKATKLSPPKLSNITAVGCIFFYATVILLGLDHSILPSAEDSF 691
Db 579 -ALATFLVLGVFVRHNATPVVKASGRELCYILLGGVFLCYCMTFFIAKPS- 629
QY 692 ATVCTARYLLSAGSFAGSMFAKTYRVHRIF--TRTGSVFKMLQDIQILILLVGGIL 749
Db 630 -GVICALRRLGVGTAFSVCYSAALLTKTNRIARIFGGAREGAQ-RPRFISPASOVAICLAI 687
QY 750 LVDALLVTLVVYTDPMERHLNLTLEISATDRSVV-YQPOVEVCRSQHTQWLSVLYAYK 808
Db 688 SGOLLIVVAVLV-----VEAPGTGKETAPERREVVTLCNHRDASMLGSLAYN 735
QY 809 GLLLVGVYMAWETRHVKIPA-LNDXOYIGVSVSVVITSATVAVVLANLISERVTLAFIT 867
Db 736 VLLIALCTLYAFKTR--KCPENFNEAKFIGTMYTTCI-----IWLAFLP 778
QY 868 ITALILTST-----TATLCL-----LFIPKLHDI 891
Db 779 I--FVVTSSDYRVQTTMCVSVLSGVSVLGCLFAPKLHII 817

RESULT 14
US-08-617-785-4
; Sequence 4, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

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Db 215 ALKNYVSTVASEGSGVEAFIQKSDGVCIAQSVKIPREPKAGEFDKIIRLLE 274
Qy 346 TDTRIIIGSFQELAPQILCBAYRLRMFGADYANILHESMGAPWPDQRTACSNHBLQLA 405
Db 275 TSNAVLIIFANEDDIRVLEAARRAQTGHFFW-----MGSDSW-GSKIAPVLHLEEVA 328
Qy 406 VENLIVSTHNSIVGNVSYSG--LNNHMFNSQLRKQSAQFHGQDGFSGSYGPRISIAAT 463
Db 329 EGAVTILPKRMSVRGDFRYFSRTLDNNRNLIWF-----AEF-WEDNFC-----KLSRHAL 379
Qy 464 QSDRRRR--RRGVVGTSGGHFLPEAISQYAPQTYDAVMAIALARAABEHW--RNEEQ 519
Db 380 KKGSHVKKCTNRERIGQDSAY-EQEGKVQF-----VIDAVYAMGHALHAMRDLCPRGVGLC 435
Qy 520 SKLDGFDYTRSDMAWEFLQMGKHLFLGVSG-PVSFS-GPDRVGTTFAYQIQ----- 569
Db 436 PRMDPVDGT-----QLLKYIRNVNFSGIAGNPVTFNENGADAPGRYDIYQYQLRNDSAEY 489
Qy 570 -----RGL-----LEPVLIY 580
Db 490 KVIQSWTDHLHLRIERMHWPGSGQQLPRISICSLPCQPGERKKTVMGMPCCWHCEPCTGYQ 549
Qy 581 PATDALDFRCPRC-----RPVWHSGOVPIAKRVEKL RVAT-----IAPLAFYTIATLSSVGI 633
Db 550 YQVDR--YTKCTCPCDMPTENRTGCRIP--IIKLEWGSNAWVLP-----FLAVVGI 599
Qy 634 A-----LAITFLAFNLHFRKKAIKLSSPKLSNITAVGCIFFVATVILLGLDHSHTLPSAED 689
Db 600 AATLVVITFVRYN-----DTPIVKASGRELSVLLAGIFLCYATTFM-----IAEP 647
Qy 690 SFATVCTARVYLLSAGSLAFGSMFAKYRVHRIETR-TGSVFKDKMLQDIQLILLVGLL 748
Db 648 DLGT-CSLRIFFLGLGMSISYAALLTKNRIYRIFEQGRKRSVAPRFISPASQLAITFSL 706
Qy 749 LLDVALLVTLWVYTPDMERHNLHLEISATDRSVV-YQOQVE-----VCRSQTQT 799
Db 707 ISQLLGLGVWFVDP-----SHSVVDFQDQRTLDPRFARGVLKDCISDL 751
Qy 800 WLSVLYAKGLLVGVYMAWETRVKIPALNDSQVIGSVYSV-VITSIAVVVL--ANL 856
Db 752 SLICLLGYSMLLWVCTVVAIKTRGV-ETENEAKPIGFTMTTCIVLAFIPIFGTSQ 810
Qy 857 ISERTVLAFTITALILSTATLCLLFPKLHDI 891
Db 811 SADKLYIQTTTLTVSVLSASVSLGLMYPKVYII 845

RESULT 12
US-08-337-797A-2
; Sequence 2, Application US/08337797A
; Patent No. 6017697
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,797A
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; FILING DATE: No. 6017697ember 14, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9431
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 872 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-337-797A-2
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Query Match 5.18; Score 340.5; DB 3; Length 872;
Best Local Similarity 21.78; Pred. No. 2.2e-21;
Matches 191; Conservative 113; Mismatches 344; Indels 233; Gaps 35;

Qy 151 GKIVLLGLFELSTSRGPRD-----GLSELGAATWAVEHNR-KRLLPG----- 193
Db 30 GDLVIGGLFPVHQKGPAEDCGPVNEHRIQRLLEAMLFALDRINRPHLLPGLVRGAHIL 89
Qy 194 -----YTLELVNTDQCDDPGVGVDRFFH-----AIYTPQSTRMVMLLGSGACSEVTE 239
Db 90 DCSKDHQALEQALDFVRSLSRGADGSRHICPDGSIYATHGDAPTATIGVIGGYSVDSI 149
Qy 240 SLAKVPYNNIVQVSGFSTSPALSDRRFFPYFYRTVPDSSHNPARIAFIRKFGMGVTT 299
Db 150 QVANLLRLFPQISYASTSAKLSKRSYDYFARTVPDPDFOAKAMAEILRFNNYTVYST 209
Qy 300 FSQNEEVHSLAVNNLVTELEAANISCAATI-----TFAATDFKEOL-LLLRETDRIIG 353
Db 210 VASEGDYGETGIEAFELEARARNI-CVATSEKVGSRASRAAFEGVVRALLQKPSARVAVL 268
Qy 354 SFSQELAPQILCEAYRLRMFGADYANILHESMGA----- 387
Db 269 FTRSEDARELLAASQRL--NASFTWASDNGGALESVVAGSEGAAGAITELASYPI 325
Qy 388 -----PW-----WPDORTACSNHLEQLAVENLIV----- 412
Db 326 DFASYFQSLDPNNSRNPFREFW-EQRFRCFRQDCAHSLRAVPFEQESKIMFVNA 384
Qy 413 -----STHNSIVGNVSYSGLNNHMFNSQLRKQSAQFHGQDGFSGYGPRIISAAT 463
Db 385 VYAMAHALHNMHRALCPNTTTLCDAMRPVNGRRLYK----DFLVNFKDAPFRP----ADT 437
Qy 464 QSDRRRRRRGVGTSGGHFLPEAISQYAPQTYDAVMAIALARAABEHWRNEEQSKLD 523
Db 438 HNEVRFDR-----FGDGIGRYNIETY-----LRAGSGRYRQKVGWAE 476
Qy 524 GFDYTRSDMAWEFLQMGKHLFLGVSGVPVPSG-----PDRVGTTFAYQIQRLLEPVA 577
Db 477 GLTLDTSLIPWASPS-----AGPLPASRSEPCQLQNEVKSVPQGEVCCWLCPICQ 526
Qy 578 LYYPATDALDFRCPRCPVKWH-----SQVPIAKRVFKLRVA-TIAPLAFYTIATLSSVG 632
Db 527 PYEYRLD--EFTCADCGLYGWPNASLTGCFELPQEIIRMGDAWAVGPV--TIACLG-- 578
Qy 633 IALAITF-LAFNLHFRKKAIKLSSPKLSNITAVGCIFFVATVILLGLDHSHTLPSAEDSF 691
Db 579 -ALATLVILGVFVRHNATPVVKASGRELCYILLGGVFLCYCMFTFFIAKPST----- 629
Qy 692 ATVCTARVYLLSAGSLAFGSMFAKYRVHRIF--TRTGSVFKDKMLQDIQLILLVGLL 749
Db 630 -GVCAIRLFGVGTAFSVCSYALLTKTNRIARIFGAREGAQ-RPRFISPASQVAICLALI 687
Qy 750 LVDALLVTLWVYTPDMERHNLHLEISATDRSVV-YQOQVECRSQHTQTWLSVLYAYK 808
Db 688 SGOLLIVVAVLV-----VEAPGTGKETAPERREVVVTLRCNHRDASMLGSLAYN 735
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; Sequence 2, Application PC/TUS9414989
; GENERAL INFORMATION:
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14989
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-14989-2

Query Match          5.2%; Score 348.5; DB 5; Length 915;
Best Local Similarity 20.4%; Pred No. 4.6e-22;
Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;

QY 148 RNHGKIVLLGLFELSTSRG-----RPDGLSELGAATMAVEHINR-KRLLPGYTL- 196
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DB 44 RIEGDVLTGLFPVHV-AKGPSVPCGDIKRENGIHRLEAMLVALQINSDDPNLNPVTILG 102

QY 197 -----ELVNTDQCDPGVGVDFRFFHAIYTOPSTRWMLLG 231
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 103 ARILDTCSDRTYALEQSLTFVQALIQKDTSDVRCTNGE-----PPVFVKPE-KVVGVI 155

QY 232 SACSEVTESLAKVPYWNIVQSFGSTSPALSDREFPYVRTVAPDSSHNPARIAFIKR 291
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DB 156 AGSSVSITWANILRLFQIPQISYASTAPELSDRRYDFFSRVPPDSFOQAQAWDIVRA 215

QY 292 FGWGTVTFTTSQNEEVHSLAVNNLVTELEAANISCAATITFAATDKFQELL-----IL 343
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 216 LGWNVYSTLASEGSYGEGVESFTQISKAEAGLCIAQSRIQPQRKDRTIDFDRIIKQLL 275

QY 344 RETDTRIIGSFOELAPOICEAYLRMFGADYAIIWHESMGAPWPDPQTACSNHELQ 403
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 276 DTPNSRAVVIFPANDEDIKOILAAAKRADQVG-HFLMWGSDSGSKINP-----LHQHE 327

QY 404 LAVENLIWSTHNSIVGNVSYSLNNHMNSOLRKQSAQFHGOBGFSGYGPRIISAAT 463
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 328 DIAGAETIQPKRATV-----EGFDAFTSKTLENNRNWFWAFYEWFENFNCKLTISSG 381

QY 464 QSDSRRRRRRGVGTSGGHLPPEAF---SQYAPQ-----TYDAVWAIALALARAEEHWR 515
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 382 KKEDTRKKTG-----QERIGKDSNYEQEKGQVVIDAVYAMAHAL-----HHMNK 427

QY 516 N-----FEQSKLDGFDYTRSDMAWEFLQOMKKHLHFLVSG-PVSFSP-GPD RVGTTA 564
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 428 DLCADYRGVCPEMEQAGG-----KKLKIRHVNFNGSAGTVPFMFKNGDAPGRYD 478

QY 565 FYQIQ-----RGL----- 572
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 479 IFQIQTTNTNPGYRLIGOWTDELQNLNTEDMQMGKGVREIPSSVCTLCKCPQORKTKQG 538

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Db 382 KKEDTRKCTG-----QERIGKDSNYEQEGKQVQFVDVAYMAHAL-----HHMNK 427
QY 516 N-----EQSKLDGFDYTRSDMAWEFLQOMGKLHFLGVSG-PVSFS-GPDRVGTGA 564
Db 428 DLADYRGVCPMEQAGG-----KKLLKYIRHVNFNGSAGTPVMKNGDAPGRYD 478
QY 565 FYQIQ-----RGL-----572
Db 479 IFQYQTNTTNPGRYRIGQWTDLQNLNEDMQWCKGVREIPSSVCTLPCKPQQRKKTQK 538
QY 573 -----LEPVALYYPATDALDFRCPRC-----RPVKWHSQ--QVPIAKRVFKLRVATIAPL 620
Db 539 TPCQWTCPCDGYQYQFD--EMTQCHQCPYDQRPNNRTGCCQNIPIIKLEWHSWAVIP--594
QY 621 AFYTIATLSSVGIATITFLAFNLHFRKKAIKLSSPKLSNITAVGCIFFVYATVILLGLD 680
Db 595 -----VFLAMGLIATIFVMATFIRYNDTPIVRASGRELSYVLLTGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFATRVYRHRIFTR-TGSVEFKDKMLQDI 739
Db 647 -----IAKPDVA--VCSFRVFLGLGMCISYAALLTKNRIYRIFEQGGKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLVWVTPDPMERHLNHLNLTLEISATDRSVVYQOQVE--VCRSQHT 797
Db 701 SQAITSLSISVQLLGVFIWFGVDP-----PNIIDY---DEHKTMPNEQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRHKIPALNDSQYIGVSYSV-VITSALVVVLANL 856
Db 753 DLQIICSLGYSILLMVTCTVYAIKTRGYP-ENFNEAKPIGFTMYTTCIVWLAFIPFFGT 811
QY 857 I--SERVTLAFITITALITLTSTATTCLLFIPLKLDI 891
Db 812 AQSAEKLYIQTTTLTISMNLSASVALGMLYMPKVYII 848

RESULT 9
US-08-176-401B-2
; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-401B-2

Query Match 5.2%; Score 348.5; DB 4; Length 915;
Best Local Similarity 20.4%; Pred. No. 4.6e-22;
Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;

QY 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSELGAATMAVEHINR-KRLPLGTYL- 196
Db 44 RIEGDVTLGLFVPH-AKGPSVGPCGDIKRENGIHRLEAMLYALDQNDPMLLPNTVLG 102
QY 197 -----ELVTNDTQCDPGVGVDFEFHAIYTOPSTRMVMLLG 231
Db 103 ARILDTCRSRTYALEQSLTFVQALIQDTSVRTNGB-----PPVFVKPE-KVGVIG 155
QY 232 SACSEVTESIAKVVYVWNIQVSEGSTSPALSDRREFFPYFRTVAPDSSHNPARTAFIRK 291
Db 156 ASGSSVSIMVANILRLFIQIISYASTAPELSDDRYDFFSRVVPPDSFQAQAMVDIVKA 215
QY 292 FPGTGVTTFSQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKEOLL-----LL 343
Db 216 LGWNVYSTLASSEGYGEGVSEFTQISKEAGGLCIAQSVRIPOERKORTIDFDRIKOLL 275
QY 344 RETDTRIIGSFQELAPOILCEAYRLRMFGADYAWILLHESMGAPWMPDQRTACSNHELO 403
Db 276 DTPNSRAVITFANDEDIKIILAAAKRADQVG-HFLWGSDSWGSKINP-----LHQHE 327
QY 404 LAVENLIVSTHNSIVGNVNSYSGLNHMFNSQLRKQSAQPHGQDGFSGSGYGPRISTAAT 463
Db 328 DIAEGAITIQPKRATV-----EGFDAYFTSRTLENNRRNVFAEYWEENENCKLTISGS 381
QY 464 QSDSRRRRRGVVGTSQGHLPPEAI---SQYAPQ-----TYDAVATALALRAAEHWR 515
Db 382 KKEDTRKCTG-----QERIGKDSNYEQEGKQVQFVDVAYMAHAL-----HHMNK 427
QY 516 N-----EQSKLDGFDYTRSDMAWEFLQOMGKLHFLGVSG-PVSFS-GPDRVGTGA 564
Db 428 DLADYRGVCPMEQAGG-----KKLLKYIRHVNFNGSAGTPVMKNGDAPGRYD 478
QY 565 FYQIQ-----RGL-----572
Db 479 IFQYQTNTTNPGRYRIGQWTDLQNLNEDMQWCKGVREIPSSVCTLPCKPQQRKKTQK 538
QY 573 -----LEPVALYYPATDALDFRCPRC-----RPVKWHSQ--QVPIAKRVFKLRVATIAPL 620
Db 539 TPCQWTCPCDGYQYQFD--EMTQCHQCPYDQRPNNRTGCCQNIPIIKLEWHSWAVIP--594
QY 621 AFYTIATLSSVGIATITFLAFNLHFRKKAIKLSSPKLSNITAVGCIFFVYATVILLGLD 680
Db 595 -----VFLAMGLIATIFVMATFIRYNDTPIVRASGRELSYVLLTGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFATRVYRHRIFTR-TGSVEFKDKMLQDI 739
Db 647 -----IAKPDVA--VCSFRVFLGLGMCISYAALLTKNRIYRIFEQGGKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLVWVTPDPMERHLNHLNLTLEISATDRSVVYQOQVE--VCRSQHT 797
Db 701 SQAITSLSISVQLLGVFIWFGVDP-----PNIIDY---DEHKTMPNEQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRHKIPALNDSQYIGVSYSV-VITSALVVVLANL 856
Db 753 DLQIICSLGYSILLMVTCTVYAIKTRGYP-ENFNEAKPIGFTMYTTCIVWLAFIPFFGT 811
QY 857 I--SERVTLAFITITALITLTSTATTCLLFIPLKLDI 891
Db 812 AQSAEKLYIQTTTLTISMNLSASVALGMLYMPKVYII 848

RESULT 10
PCT-US94-14989-2
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; Patent No. 5831047

Db 216 VSTLASEGNGVGEVFAFVQISREAGGVCIAQSIKIPREKPGFESKVIIRLMETPNARG 275
QY 352 IGFSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHELOLAVENLIV 411
Db 276 IIFANEDDIRRLEAARQANLTCGFLWVGSDSMGAKTSP-----ILSLEDVAV 324
QY 412 VSTHNSIVGNVSYGLNNHMFNSQLRKSQAQFHGQDGFSGYGPRIASIAATQSDSRRR 471
Db 325 GAI--TILPKRASIDGFDQYFMTSLNRRNIWFAEFWEENFNCKLTSSTGQSDSDSTRK 382
QY 472 RRGVGTSGGHLFPEAISQAPQTY-----DAVMAIALARAAEE-----HWRRN 516
Db 383 CTG-----EERLGR--DSTYEGEGKVQFVIDAVYAIHAHLSMHQALCPGHTGLC 430
QY 517 EEOSKIDGFDYTRSDMAWEFLOQMKGHLFLGVSG-PVSFS-GPDVRGTTAFYQIQ----- 569
Db 431 PAMEPTDG-----RMLQYIRAVRFNGSAGTPVMFNENGDPAGRYDIFQYQATNGS 481
QY 570 -----RGLLEPVALY 579
Db 482 ASSGGYQAVGQWAEITLRDVEALQWSDGPHVEVPSLCLPCGPGGERKKMKVGV--PCWH 539
QY 580 YPATDAL-----DFRCPRC-----RPVKWHSQVPIAKRVEKLRVATIAPLAFYTIATLSS 630
Db 540 CERACDGRFQVDEFTCEACDGMPTPNHTGCRTP-----VVRUSWSPPWAAPPL-LLAV 594
QY 631 VGIALATFLAFNLHFRKRLKAIKLSPPKLSNITAVGCFIVYATVILGLDHSITLPSAEDS 690
Db 595 LGIVATTVVATVRYNNTPIVRASGRKLVLLTGIFLIYAITFLM-----VAEP 645
QY 691 FATVCTARVYLLSAGFSLAFSGMFATKYRVHRIFTR--TGSVFKDKMLQDQLILLVGLL 749
Db 646 GAACVCAARLFLGLGTLSYSALLTKTNRIYRFEQGRSVTPPPFISQLVITFSLT 705
QY 750 LVDALLVTLWVYDPMERHLNLTLEISATDRSVVYQPOVE-VCRSQTQWLSVLYAYK 808
Db 706 SIQVGIITWLGARPP-----HSV--IDYEQRTVDEQARGVLLKCDMSDLISGLGIGYS 758
QY 809 GLLLVGVYMAWETRHVKIPALNDSQYIGSVYSV-VITSAIVVVLNLI--SERVTLAF 865
Db 759 LLLWVCTVVAIKARGVP-ETFEAKPIGFTMTTCIILWLAFAVPFIPTGTAQSAEKIYQT 817
QY 866 IYITALILSTTATLCLLFIPLKLDIW 892
Db 818 TLTVSLSLASVSLGFMFYVPTVIF 844

RESULT 5

US-08-617-785-14
; Sequence 14, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttnner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 922
; TYPE: PRT

; ORGANISM: Homo sapiens
US-08-617-785-14 *

Query Match 5.3%; Score 353.5; DB 4; Length 922;
Best Local Similarity 19.5%; Pred No. 1.7e-22;
Matches 201; Conservative 165; Mismatches 374; Indels 291; Gaps 40;

QY 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSELGAATMAVEHNR-KRLLPGYTL- 196
Db 44 RIEGDVTLGGLPFVH-AKGPSVPGCDIKRENGIHRELEAMVALDQINSDPNLLPNVTLG 102
QY 197 -----ELVNTDQCQDGVGVDRFFHAIYTOPSTRVMVLLG 231
Db 103 ARILDTSRDITYALEQSLTFFQALLIQKDTSDVRCNTGE-----PPVFKPE-KVGVG 155
QY 232 SACSSEVTSLAKVVPYWNIVQVSGFSTSPALSDREFFPYFRTVAPDSSHNPARIAFIK 291
Db 156 ASGSSVSIMVANILRLFIQIPQISYASTAPSELSDDRRYDFRSRVVPPDSFQAQAMVDIVA 215
QY 292 FGWGTVTTFQSEVEVHSLAVNNLVTLEAANISCAATITFAATDFKEQLL-----LL 343
Db 216 LGWNVSTLASGSGYCEKGVESFTQISKAGGLCIAQSVRIPOERKORTIDFDRIIKQLL 275
QY 344 RETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHELO 403
Db 276 DTPNSRAVVIFANDEIDIKILAAAKRADQVG-HFLWVGSDSMGSKINP-----LHQHE 327
QY 404 LAVENLIVVSTHNSIVGNVSYGLNNHMFNSQLRKSQAQFHGQDGFSGYGPRIASIA 463
Db 338 DIAEGAITIOPKRAIV-----EGFDAYFTSRTLENNRRNVWFAEYWEENFNCKLTISG 381
QY 464 QSDSRRRRRGVVGTSGGHLFPEAI--SOYAPQ-----TYDAVMAIALARAAEEHWR 515
Db 382 KKEDTRCKTG-----QERIGKDSNYEQEGKVQFVIDAVYAMAIAL-----HMMK 427
QY 516 N-----EQSKLDGFDYTRSDMAWEFLOQMKGHLFLGVSG-PVSFS-GPDVRGTTA 564
Db 428 DLCADYRGVCPMEQAGG-----KLLKYIRNVFNFSAGTPVMFNKNGDAPGRYD 478
QY 565 FYQIQ-----RGL----- 572
Db 479 IFQY 538
QY 573 -----LEPVALYYPATDALDFRCPRC-----RPVKWHSQ--OVPIAKRVEKLRVATIA 620
Db 539 TPCCWTCPCDGYQYQFD--EMTCQHCYDQRPENRTCCQDIPILKLEHSPWVIP-- 594
QY 621 AFYTIATLSSVGIATAITFLAPNLHFRKLAIKLSPPKLSNITAVGCFIVYATVILLGLD 680
Db 595 -----VFLAMLGIIATIFVMATFIYNDPTIVRASGRELSVLLTGIFLCYIITFLM--- 646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFATKYRVHRIFTR--TGSVFKDKMLQDI 739
Db 647 -----IAKPDVA-VGSFRVFLGLGMCISYAALLTKTNRIYRFEQGRKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLWVYDPMERHLNLTLEISATDRSVVYQPOVE--VCRSQT 797
Db 701 SOLAITSSLSI SVOLLGVFIWGVDP-----PNIIDY----DEHKTWNPQARGVLCDDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRHVKIPALNDSQYIGSVYSV-VITSAIVVVLNLI 856
Db 753 DLQIICSLGYSILLAVTCTVVAIKTRGV-ENFNEAKPIGFTMTTCIWLAFIPIFFT 811
QY 857 I--SERVTLAFITTTALILTSTTATLCLLFIPLKLDIWARNDIIDPVHSMGLKMECNR 914
Db 812 AQSAEKLYIQTTLTISMNLSASVALGMLYMPKVII-----IFHP----- 852
QY 915 RFVVDRELOYRVQVNVYKKEIQALDAEIRKLERLLESGLTTSITTSSTSLTGG 974
Db 853 -----ELNVOKRRSRFAVVTA----- 869
QY 975 CHLAKPELTVTSGISQTPAASKN--RTPSISGILPNLLISVLPVPIPRASWPSAEYMOIP 1031

; Sequence 2, Application US/08407875
; Patent No. 5912122
; GENERAL INFORMATION:
; APPLICANT: Dagget, Lorrie
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; SUBTITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08407875
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9921
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 877 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-407-875-2

Query Match 5.5%; Score 372; DB 2; Length 877;
Best Local Similarity 21.6%; Pred. No. 3.2e-24;
Matches 187; Conservative 132; Mismatches 364; Indels 182; Gaps 30;

QY 151 GKIVLLGLFEL-----STSRGP--RPDGLSELGAATMAVEHINR-KRLPLG----- 193
DB 37 GGLTLGLFPVH-ARGAAGRACGQKKEQGVHREAMLYALDRVADNADPELLPGVRLGARLL 96

QY 194 -----YTLELVNTDTC-----DPGVGDVDRFFHAIYTOPSTRMVLMLGSAACSEV 237
DB 97 DTCSDRTYALEQALSFVQALLIRGRGDGVGRCGPGVPLRPAPPERRVAVVVGASASSV 156

QY 238 TESLAKVVPVWNIQVSGSTSPALSDRRFFPYFTVADPSHNPARIATFKKFGWTV 297
DB 157 SIMVANVLRFAIPQISYASTAPELSDTRYDFSRVVPDPDSYQAQAMVDIVRALGWNIV 216

QY 298 TTFQNEEVHSLAVNNLY-TELEAANISCAATITFAAT-----DFKEQLLLRETDRII 352
DB 217 STLASEGNGSGGVDAFVQISREAGVCVIAQSIKIPREPKEGFSKIVIRLMETPNARGI 276

QY 353 GSFQELAPQILCEAYRLRMFGADYAWILHSMGAPWPPDQRTACSNHLEQLAVENLIV 412
DB 277 IIFANEDDIRRVLEAARQANLTGHLWVGSDSWGAKTSP-----ILSLEDVAVG 325

QY 413 STHNSIVNNVSYGLNNHMFNSQLRKSQAOPHGQDGFSGYGPRTISAATSDSRRRR 472
DB 326 AI--TILPKRASIDGDFQYFMTSRLENRRNIWFAEFWEENFNCKLTSSGTSQSDSTRKC 383

QY 473 RGVVGTSGCHLPPEAISQAPQTY-----DAVNIALALRAEE-----HWRRNE 517
DB 384 TG-----EERIGR--DSTYBQEGKVQFVIDAVYAIHAHALSHMHQALCPGHTGLCP 431

QY 518 EQSKLDGFDYTRSDMAWEFLQOMGKHLFLGVSG-PVSFS-GPDRVGTATFAVQIQ----- 569
DB 432 AMEPTDG-----RMLLOYIRAVRFGSAGTVMFNENGDPAGRYDIFQYQATNGSA 482

QY 570 -----RGLLEPVALYY 580
DB 483 SSGGYQAVGQWAEITRLRDVEALQWSDPHEVPSSLSLPCGPGERKKMKVGV--PCWHC 540

QY 581 PATDAL-----DFRCPRC-----RPVKHWSGVPIAKRVFKLRVATIAPLAFYTIATLSSV 631
DB 541 EACDGYRFQVDEFTCEACPCGDMRPTNHTGCRPTP-----VVRLSWSSPWAAPPL-LLAVL 595

QY 632 GIALAITFLAFNLHFRKKAIKLSSPKLSNITAVGCIFTVATVILLGLDHSHTLPSADSF 691
DB 596 GIVATTTVATFVRYNNTPIVRASGRELSVLLTGIFLIYAITFLM-----VAEPG 646

QY 692 ATVCTARVYLLSAGFSIAFGSMFAKTYVRHRIETR-TGSVFKDKMLQDIQLILVGGILL 750
DB 647 AAVCAARLFLGTLTSLYSALTKTNIYRIPEQGRSVTPPPFIPTSOVLVTFSLTS 706

QY 751 VDALLVTLVWVTPDMERHLHLNLTLEISATDRSVVYQVQE-VCRSQHTQTWLSVLYAYKG 809
DB 707 LQVVGMIWLARGPP---HSV---IDYEQRTVDPEQARGVLKCDMSDLSLCLGYSL 759

QY 810 LLLVGVYVMAWETRHVKIPALNDSQYIGSVYSV-VITSALVVVLANLI--SERVTIAFI 866
DB 760 LLMVTCVYAIKARGVP-ETFNKAPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYIQT 818

QY 867 TITALLITSTTATLCLLFIPLKLDI 891
DB 819 TLTVSLSLSASVSLGMLYVPKTYVI 843

RESULT 4
US-09-126-280-2
; Sequence 2, Application US/09126280
; Patent No. 6103524
; GENERAL INFORMATION:
; APPLICANT: Wu, Su
; APPLICANT: Belagaje, Rama M
; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic
; FILE REFERENCE: Acid
; FILE REFERENCE: Sequence List
; Patent No. 6103524
; CURRENT APPLICATION NUMBER: US/09/126,280
; CURRENT FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 877
; TYPE: PRT
; ORGANISM: Human
; US-09-126-280-2

Query Match 5.5%; Score 371; DB 3; Length 877;
Best Local Similarity 21.5%; Pred. No. 4e-24;
Matches 186; Conservative 133; Mismatches 364; Indels 184; Gaps 30;

QY 151 GKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLPLG----- 193
DB 37 GGLTLGLFPVH-ARGAAGRACGQKKEQGVHREAMLYALDRVADNADPELLPGVRLGARL 95

QY 194 -----YTLELVNTDTC-----DPGVGDVDRFFHAIYTOPSTRMVLMLGSAACSE 236
DB 96 LDCSRDRTYALEQALSFVQALLIRGRGDGVGRCGPGVPLRPAPPERRVAVVVGASASS 155

QY 237 VTESLAKVVPVWNIQVSGSTSPALSDRRFFPYFTVADPSHNPARIATFKKFGWGT 296
DB 156 SIMVANVLRFAIPQISYASTAPELSDTRYDFSRVVPDPDSYQAQAMVDIVRALGWNV 215

QY 297 VTFQNEEVHSLAVNNLV-TELEAANISCAATITFAAT-----DFKEQLLLRETDRII 351
DB 819 TLTVSLSLSASVSLGMLYVPKTYVI 843

Matches	253;	Conservative	152;	Mismatches	304;	Indels	200;	Gaps	19;
QY	155	LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKRLLPGYTLLELWNTDQDGPVGVDRF	214						
Db	43	IMGMLPTKEVAGSGIGRGVLPAVELATEQIRNESLRLPYFLDLRLXYTECDNAGLKAF	102						
QY	215	FHAIYTOPTRWMLLGSACSEVETSLAKVYPYNNIVOVSGSTSPALSDRRPEPYFRT	274						
Db	103	YDAIKYGN--HLMVFGVCPVSTIAETSLQGWNLVOLSFSAATTPVLADKKKPYFFRT	160						
QY	275	VAPDSSHHPARIAFLRKFGWGTVTTFSONEEVHSLAVNNLVEEAAINCAATITPA--	332						
Db	161	VPSDNVNPALIKLLKHQWRKRGTLTDVORFSEVRNLTGLVGEDIEDIESFESND	220						
QY	333	-ATDFKEOLLRLRETDRILIIIGSFSEQLAPQILCEAYRLRMFGADYAWILHESMGAPWP	391						
Db	221	PCTSVKK---LKGNDVRIILGQFDONNAKVFC-----	250						
QY	392	DORTACSNHELQAVENLIVVYSTINSIVGNVSYSGLNHMFNSOLRKQSAQFHQDQFG	451						
Db	251	-----CTPOQYEREYNNK-----	264						
QY	452	SGYGPRIISAATQSDSRRRRRGGVGTSGGHLFPEALISQAPQYDAVWATALARAE	511						
Db	265	SGVG-----SKFHGYADGLWIAKTLQRAHE	292						
QY	512	HWRNEEQSKLDGDDYTRSDMAWEFLQOMKLHFLGVSGPVSFSDPRDVGVTAFYQIQRG	571						
Db	293	TLHASSRHORIODEYTDHTLGRILNAMNETNFGVTQGVVFRNGERMGTIKFTQFQDS	352						
QY	572	LLEPVALYPATDALDFPCPRCPYKHKSGOVPIAKRVFKLRVATIAPLAYTIATLSSV	631						
Db	353	REVKGVEYNADVLEIIND--TIRFGSEPPPKDKTILILSOLRKISLIPIYSIISALTIL	409						
QY	632	GIALAITFLAFLNHFRLKAIKLSGPKLSNTAVGCIFFYATVILGLDHSITLPSAEDSF	691						
Db	410	GMINASALFFNKNRROKLIKMSPYMNNLIIIGMLSYASIEFLGLDGSFV--SEKTF	467						
QY	692	ATVCTARYLLSAGFSIAFGSMFAKTYRVHRIFTRTGSVFKDKMLQDILQLIVGGLLV	751						
Db	468	ETLCTVTRTWILTGTGTTAFGAMFAKTRVHAIFKNV--KMKKKIKIDQKLLVIVGMLLI	525						
QY	752	DALLVTLWVYTDPMERHLNHLTLEISATDRSVVYQPOVEVCRSOTHTWLSVLVAYKGLL	811						
Db	526	DLCLILICQAVDPURRIVEKYSMEPPDPAGRDISIRPLEHCENTHMTIWLGIIVYAYKGLL	585						
QY	812	LVGVYMAWETRHVKIPALNDSQYIGVYSVSWITSAIVVVLNANLISERVTLAFITITAL	871						
Db	586	MLFCFLAWETRNVYSIPALNDSKVLGMSVYNGIWCIIAGAVSFLTRDQPNVQFCIVALV	645						
QY	872	ILTSTTATLCLLFIPIKLHDIAWRNDIIDPVIHSMGLKMECNTRRFVDDRELQYRVEVQ	931						
Db	646	IIFCSTITLCLVFVKL-----ITLRTNPDAAQTQNRKFQ---TQ	682						
QY	932	NRVYKKEIQALDAIRKLERLLESGLTTSTTT--SSSTSLITG---GGHLKPELT---	982						
Db	683	NQ--KK-----EDSKTSTSVTSVNOASTSRLEGLOSENHRLRKIKITELD	724						
QY	983	-----VTSGISQTPAASK-----NRTPTISG---ILPNLLLSVLPPVI	1017						
Db	725	KDLEEVTHQLODTPKTYIKONHYQELNDILNGNTFESTDGGKALKLNHL-----DQN	779						
QY	1018	PRASWPSAE	1026						
Db	780	POLOWNTE	788						

Qy	821	ETRHVKIPALNDSQYIGSVYSWITS	847
Db	294	ETRNVSIPALNDSKYIGMSVYNVGIIIS	320

RESULT 3
US-08-407-875-2

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1  APPLICANT: STAMMERS, MELANIE
2  TITLE OF INVENTION: NOVEL COMPOUNDS
3  NUMBER OF SEQUENCES: 4
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Ratner & Prestia
6  STREET: P.O. Box 980
7  CITY: Valley Forge
8  STATE: PA
9  COUNTRY: USA
10 ZIP: 19482
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: DOS
15 SOFTWARE: FastSeq For Windows Version 2.0
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/183,253
18 FILING DATE: 30-OCT-1998
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 9817907.0
22 FILING DATE: 17-AUG-1998
23 APPLICATION NUMBER: 60/075,306
24 FILING DATE: 20-FEB-1998
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Prestia, Paul F.
27 REGISTRATION NUMBER: 23,031
28 REFERENCE/DOCKET NUMBER: GP-70395
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 610-407-0700
31 TELEFAX: 610-407-0700
32 TELEX: 846169
33 INFORMATION FOR SEQ ID NO: 4:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 332 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 US-09-183-253-4
41
42 Query Match 8.88; Score 588.5; DB 3; Length 332;
43 Best Local Similarity 36.7%; Pred. No. 1.7e-44;
44 Matches 120; Conservative 74; Mismatches 126;
45 Indels 7; Gaps

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;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:04:59 ; Search time 26.74 seconds
(without alignments)
1098.235 Million cell updates/sec

Title: US-09-715-962-6
Perfect score: 6705
Sequence: 1 MKIIQPVQTRYGPWPVGL.....RLSLGDSQEEEQAPANGTE 1305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	976	14.6	859	3 US-09-183-253-2	Sequence 2, Appli
2	588.5	8.8	332	3 US-09-183-253-4	Sequence 4, Appli
3	372	5.5	877	2 US-08-407-875-2	Sequence 2, Appli
4	371	5.5	877	3 US-09-126-280-2	Sequence 2, Appli
5	353.5	5.3	922	4 US-08-617-785-14	Sequence 14, Appli
6	349.5	5.2	915	4 US-08-617-785-12	Sequence 12, Appli
7	348.5	5.2	915	1 US-08-453-882-2	Sequence 2, Appli
8	348.5	5.2	915	2 US-08-452-734A-2	Sequence 2, Appli
9	348.5	5.2	915	4 US-08-176-401B-2	Sequence 2, Appli
10	348.5	5.2	915	5 PCT-US94-14989-2	Sequence 2, Appli
11	347	5.2	912	4 US-08-617-785-2	Sequence 2, Appli
12	340.5	5.1	872	3 US-08-337-797A-2	Sequence 2, Appli
13	340.5	5.1	872	3 US-09-258-523-2	Sequence 2, Appli
14	339	5.1	867	4 US-08-617-785-4	Sequence 4, Appli
15	336.5	5.0	908	4 US-08-855-146-2	Sequence 2, Appli
16	336	5.0	912	5 PCT-US91-09422-19	Sequence 19, Appli
17	328.5	4.9	908	3 US-08-823-110-1	Sequence 1, Appli
18	328.5	4.9	908	3 US-08-604-298-1	Sequence 1, Appli
19	324	4.8	1219	2 US-08-687-289A-6	Sequence 6, Appli
20	323	4.8	879	1 US-08-072-574-6	Sequence 6, Appli
21	323	4.8	879	1 US-08-486-270-6	Sequence 6, Appli
22	323	4.8	879	3 US-08-367-264-6	Sequence 6, Appli
23	262	3.9	1059	4 US-09-134-513-2	Sequence 2, Appli
24	257.5	3.8	1199	1 US-08-041-538-2	Sequence 2, Appli
25	257.5	3.8	1199	1 US-08-463-642-2	Sequence 2, Appli
26	257.5	3.8	1199	1 US-08-455-602-2	Sequence 2, Appli
27	257.5	3.8	1199	2 US-08-465-157-2	Sequence 2, Appli

28	257.5	3.8	1199	5 PCT-US91-09422-2	Sequence 2, Appli
29	243.5	3.6	1056	2 US-08-687-289A-7	Sequence 7, Appli
30	242	3.6	1194	4 US-08-538-526-1	Sequence 1, Appli
31	240	3.6	1085	1 US-08-485-588-5	Sequence 5, Appli
32	240	3.6	1085	1 US-08-484-565-5	Sequence 5, Appli
33	240	3.6	1085	2 US-08-480-751-5	Sequence 5, Appli
34	240	3.6	1085	2 US-08-943-986-5	Sequence 5, Appli
35	240	3.6	1085	3 US-08-353-784-5	Sequence 5, Appli
36	240	3.6	1085	3 PCT-US91-09422-17	Sequence 17, Appli
37	237	3.5	906	5 US-08-484-719B-5	Sequence 5, Appli
38	237	3.5	1078	1 US-08-485-588-7	Sequence 7, Appli
39	237	3.5	1078	1 US-08-484-565-7	Sequence 7, Appli
40	237	3.5	1078	2 US-08-480-751-7	Sequence 7, Appli
41	237	3.5	1078	2 US-08-943-986-7	Sequence 7, Appli
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43	237	3.5	1078	3 US-08-484-719B-7	Sequence 7, Appli
44	233.5	3.5	1088	1 US-08-485-588-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-2

Query Match 14.6%; Score 976; DB 3; Length 859;
Best Local Similarity 27.8%; Pred. No. 1.le-78;

Search completed: April 30, 2002, 10:06:25
Job time: 393 sec

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Qy 865 FITTALLTSTTATLCLLPDKLHDW---ARNDIIDPVIHSMGLMKMCNT--RRFVVD 919
Db 842 -----LAAAFGLLACIFFNKVYIILFKPSRNTIE-----VRCSTAAHAFKVA 885
Qy 920 DRRELOVRVEQNRVYKKEIQALDAEIRKLERLLESGLTTTSTTSSSTSLTGGGHLKP 979
Db 886 ARATLR-----RSNVSRORSSSLGG-----STGSTPSSSTSSKSNSDEDPFP 926
Qy 980 ELTVTSGISQTPAAKKNRTPSISGILPNLLSVLP-----PVIPRASWPSAEYMQIDPM 1032
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Qy 1033 RR-----SVTFA---SQPO-----LEEACLPADQLINLRLAHQ-----1062
Db 969 CKQKVFSGTWTFSLSFDEPOKTAVAHRNSTHOTSLEAKKNDALTKHQALLPLQCGT 1028
Qy 1063 --QATEAKTGL 1071
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RESULT 15
A56715
calcium receptor (clone pHCaR-4.0) - human
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
C;Accession: A56715; S49341; A49419; B49419; C49419
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
A;Reference number: A56715; MUID:95279439
A;Accession: A56715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1078 <GAR>
A;Cross-references: GB:U20759; NID:9683744; PIDN:AAA86503.1; PID:9683745
R;Pearce, S.H.S.; Thakker, R.V.
submitted to the EMBL Data Library, August 1994
A;Reference number: S49341
A;Accession: S49341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>
A;Cross-references: EMBL:X81086
R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,
Cell 75, 1297-1303, 1993
A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric
A;Reference number: A49419; MUID:94094324
A;Accession: A49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 178-192 <POL>
A;Experimental source: family N
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and ne
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
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A;Status: preliminary
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A;Residues: 289-303 <PO2>
A;Experimental source: family E
A;Note: sequence modified after extraction from NCBI backbone
A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and ne
A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
A;Accession: C49419
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 788-802 <PO3>
A;Experimental source: family J
A;Note: sequence modified after extraction from NCBI backbone

A;Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and
A;Note: sequence extracted from NCBI backbone (NCBIN:142457)
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 3.5%; Score 237; DB 2; Length 1078;
Best Local Similarity 19.9%; Pred. No. 4e-08;
Matches 201; Conservative 141; Mismatches 373; Indels 296; Gaps 44;

Qy 143 PAEMQRNHRGKIVLGLFEL-----STSRGPRPD-----GLSELCAAMAVEHI 185
Db 22 PDQRAQKKGDIILGGLFPIHFGVAAKDODLKSREPSEVICRYNFERGFQWLOAMIFATEI 81
Qy 186 NRK-RLPLVGYTLELVNDTQCD-----PGVGVDFFFHAIYTPQSTRM 226
Db 82 NSSPALLPLNTLGVRIYFDT-CNTVSKALEATLSEVAQNKIDSLNDEFNCSEHIPST-- 138
Qy 227 VMLLGSACSEVTESLAKVPYWNIVQVSGSTSPALDRREFPYFYRTVAPDSSHNPARI 286
Db 139 IAVVGATGSGVSTAVANLLGLFYIPQVSYASSSLLSNKQKFLRTPINDEHQATAMA 198
Qy 287 AFIRKFGWGTWTFSONEEVHSLAVNLTVELEAANISCAATITFAATDFKEQL----- 340
Db 199 DIIEYFRNWNVGTIAADDDYGRPGIEKFEAEERDI-----CIDFSELISQVSD 249
Qy 341 -----LLRETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMPD 392
Db 250 EEIQHVVEVIQNSTAKVIVVFSSGPDLEP-LIKEIVRNITGK-IWLASEA-----W- 299
Qy 393 QRTACSNHELQLAVENTLVSTHNSIVGNVYS-----GLNHHM-----F 433
Db 300 -----ASSLIAMPQVPHVVGTTGTFALKAGQIPGFREFLKKVHPKRSVHNGF 347
Qy 434 NSOLRKOSAQFHGQDG-----FGSGY--GPRISIAATQSDSRRRRRRGVVGTSGG 481
Db 348 AKFEWEETFNCHLOEGAKGKPLPVDTLRGHEESGDRFSNSTAFRPL-----CTGD 398
Qy 482 HLFPEALISQYAPQ-----YDAVMAIALALR-----AAEHHW 513
Db 399 ENISSVETPYIDYTHLRISYNYLAVYSIAHALQDIYTCPLGRGLFTNGSCADIKKVEAW 458
Qy 514 RNREEQSKLD-----GFDY-----TRSDMAWEFLQMG----- 541
Db 459 QVLKHLRLHNAFTNMGEQVTFDECGDLGVNYSIINWHLSPEGDSIVFKEVGYNYVYAKKG 518
Qy 542 -----KLHFLGVSGPVFSFGPDR--VGTTAFYQIQRGLLE-----PVAL 578
Db 519 ERLFINEEKILWSGFSREVPFNSCRDLACT-----RKGIIEGPTCCFECVECPDGE 572
Qy 579 YYPATDALDFRCPCRPVKW---HSGQVPIAKRVFKLRVATIAPLAFYTTATLSSVGVIA 634
Db 573 YSDETD--SACNKCDDDFWSNENHTS--CIAKEIEFLSWTEPGIALTLFAVL--GIF 625
Qy 635 LATFTLAFNLHFRKKAIKLSSPKLSNITAVGCIFFVATVILLGLDHTSLPSAEDSFATV 694
Db 626 LTAFLVLGVFKFRNTPIVKATNRNLSYLLLFSLCCFSSSLFF-----IGEPQD--WT 676
Qy 695 CTARVYLLSAGFSLAFGSMFAKTVRHRIF--TRTGSVFCKMLODIQILLLVGGLLLVDA 753
Db 677 CRURQPAFGISFVLICISILVKTNRVLLVFEAKIPTSFHRKRWGLNLQFLVFLCTFMOI 736
Qy 754 LLVTLVWVWTD-----MERHLNLTLEISATDRSVYVQVQVEVCRSQHTQTWLSVLYAYKG 809
Db 737 VICVIMLYTAPPSSYRNQOEDELEIFTCHEGSLMA-----LGLFITYC 781
Qy 810 LLLVGVYMAWETRHRVKIPA-LNDSQYIGVS--VYSVVITS---AIVVLANLISERVTL 863
Db 782 LLAACIFFFAFKSR--KLPEFNEAKRFTFMSLFFIVWISFIPAYASTYCKFVSAVEVI 839
Qy 864 AFITITALLTSTTATLCLLPDKLHDW---ARNDIIDPVIHSMGLMKMCNT--RRFVW 918
Db 840 A-----LAAAFGLLACIFFNKVYIILFKPSRNTIE-----VRCSTAAHAFKV 883

Db 311 DVTGQYRE-AVGSIITIKLQSPDKWFDYLLKLPETNLRNPNWFQEFQWHRFOCRU--- 366
QY 441 SAOFHQDGF---GSGYGPRISTAQSDSRRRRRVVGTSGLHPEALISQYAPQTYD 497
Db 367 -----EGFAQNSKYN-----KTCNSSILTRTHVQDSKMGFVI-----N 401
QY 498 AVWAIALARAEEHRRNEEQSKLQGF---DYTRSDMAWEFLQOMKGLHFLGVSGPV- 552
Db 402 AIYSMAVGL-----HNMQMSLCPYAGLCLDAMKPIDGRKLLDLSMKNTFTGVSGDMI 453
QY 553 -----SFGSGPDR-----VGTAFYQIQRG-----LLEP 575
Db 454 LFDENGDSRGYEIMFEKEMGKDYFDYINGSWDNGELKMDDEWVKNNIIRSVCSPE 513
QY 576 -----VALYYPATDAL-----DFRCPRCPVKWHSQ-----VPIAKRV 609
Db 514 CEKGQIKVIRKGVSCWCTPCKENEYVEDEVTCKACQLGSWPTDGLTGCDLIPVQ--- 570
QY 610 FKLRVATIAPLAFYTTATLSSVGLAALTEFLAFLNHLRKLKAIKLSPKLSNITAVG-CI 668
Db 571 -YLRWGDPEPIAAVFACL---GLLATLFTVFIIRYROTTPVVKSSRELCYIILAGICL 626
QY 669 FVYATVILLGLDHLSTLPSAEDSPATVCTARVYLLSAGFSL---AFGSMFAKTYRVHRIF 724
Db 627 GYLCTCLI-----AKPQIYCYLQRIQIGILSPAMYSALYTKTNRIARIL 672
QY 725 TRFGSVFKDK---MLQDIQLILLVGLLVDALLVTLVWVTPDMERHLNHLTLEISATD 780
Db 673 AGSKKICTKKPRFMSACALVIAFILICIQGLIIVAFIMEPDDIMHDYPSIREVYL-- 730
QY 781 RSVVYQPOVEVCSQHTQWLVLVYAYKGLLLVGVYMANETHRVKIPA-LNDSQYIGVS 839
Db 731 -----ICNT---TNLGVVTPLYGGLLILSCTFYAFKTRNV---PANFNEAKYIAFT 776
QY 840 VYXSV-VITSAVVVLANLISERVTLAFITITLITLITTTATLCLLTPKLDHIWARNDII 898
Db 777 MYTTCILWIAFVPIYGSNKYIITMCF---SVLSATVALGC-MFVPKVYIILA----- 826
QY 899 DVIHSMGLKMECNTRFRVVDREQLRYVEVQNRVYKKEIQALDABIRKLERLLESGLT 958
Db 827 -----KPERNVRSAFT---TSTVVRMHVGDGKSSSAASRSSSLVNLWKRGSSGET 874
QY 959 TWS---TTTSSSTSLTGGHKLPELTV-----TSGISQTPAASKNRPSPIS--- 1002
Db 875 LSSNGKSVTWAQNEKSTRGOHLQWRLSVHINKKENPNQTAIVIRFPKSTENRGFGAAAG 934
QY 1003 GILPNL-----LLSVLPVPIPRASWPSAEYMQIPMRRSVTFASQPLEEACLPADLI 1055
Db 935 GSGPGVAGNAGNACTATGGPEPPDAG-PKALYDVAEAESEFPAAARSPSPFI----- 986
QY 1056 NLRLAHQQAATEAKTGLINLRGIFSRITSSNKGSTASLADQKGLKAAFKSHMGLFTRLIP 1115
Db 987 -TSLSHLAGSAGRTD--DDAPSLHSETAARSSSSQGSIMEQ-----I 1025
QY 1116 SGTASCNALYNNPNODSPSEASSHPNGNHLKPIIRGSLTKSGTHL-DHLTKDPNELPI 1174
Db 1026 SSVVTRFTANISELNSMLSTAAATGPPGT---PICSSYLIPKEIQIPLTTMTTFAEIQPL 1082
QY 1175 PFI--SGGEGQDQTLGGKVKVLLKLVNLFOLPSNRPSVVQ---PSLREVRGSPREP 1229
Db 1083 PAIEVTVGAAGQ-----ATGVS---PAQETPTGAESAPGRPDLEELVALTTPSP 1127
QY 1230 HR 1231
Db 1128 FR 1129

RESULT 14

S40476

Ca(2+)-sensing receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C:Accession: S40476

R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.
Nature 366, 575-580, 1993
A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor fro
A:Reference number: S40476; MUID:94077182
A:Accession: S40476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1085 <BRQ>
A:Cross-references: GB:S67307; NID:g453108; PIDN:AAB29171.1; PID:g453109

Query Match 3.6%; Score 240; DB 2: Length 1085;
Best Local Similarity 20.0%; Pred.No.2.5e-08;
Matches 230; Conservative 153; Mismatches 412; Indels 356; Gaps 53;

QY 143 PAEMQRHGKIYLLGLFEL-----STRGPRPD-----GLSLGAATMAVEHI 185
Db 23 PDQRAQKGDILGLGFLPHFGVAKVQDQDLKSRPSEVICRYNFRGFWLQAMIFAIEI 82
QY 186 NRK-RLLPGYILELVNDTQCD-----PGVGVDRFFHAIYTPQSTRM 226
Db 83 NSSPALLPNMTILGYRIFDT-CNTVSKALEATLSFVAQNKIDSLNLDKFCNCSEHIPST-- 139
QY 227 VMLGSAESVETESLAKVVPYWNIVQVSGSTSPALSDRRPEFYRTVAPDSSHNPARI 286
Db 140 IAVGATSGSIGSTAVANLLGFLYIPQVSYASSRLLSNKQKSFRLTIPNDEHOATAMA 199
QY 287 AFIRFGGTVTTFQNEEVHSLAVNNLVELEAANISCAATITFAATDFKQL----- 340
Db 200 DIIEFRNNWGTIAADDYGRPGIEKPREAEERDI-----CIDFSLISQYSDE 250
QY 341 -----LLRETDTRIIGFSQELAPQILCEAYRUMFGADYAWILHESMGAPWMPD 392
Db 251 EKIQVQVEVIQNSTAKVIVWFSSGPDLEP-LIKEIVRRNITGR--IWLASEA-----W-- 300
QY 393 QRTACSNHELQAVENLIVVSTHNSIVGNVSYSLN-----NHM 432
Db 301 -----ASSLIAMPEYFHVVGTTGF-GLKAGQIPGFRFLQKVHPRKSVHNG 347
QY 433 FNSQLRKQSAFHGQDG-----FGSGY---GPRISIAATQSDRRRRRRVVGVTSG 480
Db 348 FAKFEWETFNCHLQEGAKGPLVDTFILRGHEEGGARLSNSPT---AFRPLCTGENISS 404
QY 481 -----GHLPPEAISQAPQTYDAVWAIALALR-----AAEEH 512
Db 405 VETPYMDYTHL-----RISYNVYLVAVYSIAHALQDIYTCIPGRGLFTNGSCADIKKVEA 458
QY 513 WRNREEQSKLD-----GFDYTRDMA-----WFLQOMG----- 541
Db 459 WQVLKHLRLHNLFTSNMGEQVTFDEC-GDLAGNYSTIINHLSPEDEGSIVFKEVGYNNVYAK 517
QY 542 -----KLHFLGVSGPVSGPDR---VGTTFAYQIQRGILLE-----PV 576
Db 518 KGERLFINDEKILWGSFREVFPFSCNRDCLAGT-----RKGLIEGEPTCCFEVCEPD 571
QY 577 ALYYPATDALDFRCRCRPVKW---HSGQVPIAKRVFKLRVATIAPLAFYTIATLSSVG 632
Db 572 GEYSDETTA---SACDKCPDDEWSNENHTS--CIAKEIEFLSWTEPFGIALTLFAVL--G 624
QY 633 IALAITFLAFLNHLRKLKAIKLSPKLSNITAVGCIFFVATVILLGLDHLSTLPSAEDSEA 692
Db 625 IFLTAFVLGVFIKFRNTPIVRKATNRELSYLLLSLCCFSSSLFF-----IGEPQD--- 675
QY 693 TVCTARVYLLSAGSFSAFGSMFAKTYRVHRIF-TRTGSVEKDKMLQDIQLILLVGLLLV 751
Db 676 WTCRLRQPAFGISFVLICISILVKTNRVLLVFEAKIPITSFHRKWWGLNLQFLVFLCTFM 735
QY 752 DALLVTLVWVTPDMERHL-HNLTLAISATRSVVYQPOVEVCSQHTQTLVSLVYAKGL 810
Db 736 QIVICAIWLNTPASSYRNHELEDEI-----IFITCHEGSLMALGFLIGYTCL 783
QY 811 LLVGVGVYMANETHRVKIPA-LNDSQYIGVS--VWSVWITS---AIVVVLANLISERVTLA 864

Nature 349, 760-765, 1991
A:Title: Sequence and expression of a metabotropic glutamate receptor.
A:Reference number: S15362; MUID:91136047
A:Accession: S15362
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: q-1199 <MAS>
A:Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1; PID:g56647
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.8%; Score 257.5; DB 2; Length 1199;
Best Local Similarity 19.9%; Pred. NO. 1.7e-09;
Matches 249; Conservative 171; Mismatches 459; Indels 375; Gaps 57;

Qy	120	LNLP	PPRORYLKVNOVFESERRMSPAEMQRNHGKIVILGLFELSTSRGPRD-----	170
Db	16	MSIL	PPRDPKRVLLAGASSOR---SVARMGDOVITCALF--SVHHQPAEKVPERKCGE	69
Qy	171	----	GLSELGAAATMAVEHINRKR-LLPGVTLFELVNDTQC-----	205
Db	70	IREQ	GIQRVEMFHTLUDKINADPVLNPNTILGSEIRDS--CWHSVALSQSIEFIRDSLI	128
Qy	206	----	DPGVGRDFRHAIYTOPSTR-----MVLMLGSAGSEVTESLAKVVPWNIVQVSFGST	258
Db	129	SIRDE	KDGLNRCLPDGOQLPPGRTKPKIAGVICPGSSVAIQVQLQLDFDIPQIAYSAT	188
Qy	259	SPALSD	RRPEFPYFVRTVAPOSSHNPIARIAIRKFGNGTVTTFQSENEEVHUSLAVNNLVTEL	318
Db	189	SIDLS	DKTLKYFLURVVPSTQLAARMLDVIKKRYNW--TVSAVHTGNTGESGMDAFKEL	247
Qy	319	EAANIS	CAATITTTAATDFEKOLL--LLRETDTRI---IIGFSQELAPQILCEAVR---	369
Db	248	AAQEG	LCIAHSDKIYSNAGEKSFDRLLKRLRELPKARVVVCEGTVRGLLSAMRRLG	307
Qy	370	----	LRMEGADYAWI-----	388
Db	308	VWGEF	SLIGSD-GWADRDEVIEGVEANGGITIKLQSEPVRSFDDYFLKRLDTRNRP	366
Qy	389	WWPD-	--QRTACSNHLEQLAVENLIVVSTHNSIVGNVNSYGLNNHMFNSQLRKQSAQPH	445
Db	367	WFPE	FWHRFQCRPLPGHLLNPNFKVKVCTGNELEENYODSKMGFVINAIY-----	422
Qy	446	QDGF	FGSGYGB---RISIAATQSDSRRRR---RRGVGVTSGHLFPEALISQVAPOTYDA	498
Db	423	GLQNH	HALCPGHVGLCDAMKPIDGRKLLDFLTKSSFVGSVEGFDEKGD-APGRYDI	481
Qy	499	VWATA	LALRAAEHRRNEEQSKLDGFDYTRSDMAW-----EFLQMGKLHFL-GVS	549
Db	482	M----	-----NLQVTEANRYDYHVHG--TWHEGVNLIDDYKIQMKNKSGMVRVSC	524
Qy	550	GPVSF	SPDRVGTTFATQIQGLLEPVALIYPATDAL-----DFRCPRCPVKVHSSQ	602
Db	525	SEPC	CKGQIKV-----IRKG---EVSCCWICTACKENEFODEFTCRACDLGWPNPAE	574
Qy	603	V----	PIAKRVFKLR-VATIAPLAFYTIATLSSVGIATLITFLAFNLHFKRLKAIKLSPP	657
Db	575	LTGCE	PIPVRYLEWSDIESIIATAF-----SCGLILVTFLFVLIRDPVPVKSRR	628
Qy	658	KLSNI	TAVGCIFFVATVILGLDHSITLPSAEDSFATVCTARVVLISAGFSLAFSGSMFAKT	717
Db	629	ELCV	IILAGIFLGVCPFTLIAKPTT-----TSCYLQRLVGLISSAMCYSAIUVTKT	679
Qy	718	YRVRI	EFTRGS-----VFKDKMLODIQLILLVGLLLVD-ALLVTLVWVTDMEHRLHN	771
Db	680	NRIAR	IL--AGSKKKICTRKPFRMSAWAQVIAISILISVOLTIVLVTIIMEPPM-----	731
Qy	772	LTLAIS	ADRSVVYQPOVE-----VCRSOHTQTLWSVL--YAYKGLLLVGVVYMAWETRV	825
Db	732	-----	PILSPSIKEVWILICNTSN-----LGVVAPVGYNGLLIMSCITYYAFKTRNV	777
Qy	826	KIPA-	LNDSQIYGSVYSV-VITSAIYVVLVLANLISERVTLAFITITIALITSTATLCLL	883

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Db 778 --PANFNEAKYIAFTMYTTCIIWLAVVPYIFGSGNYKIITCF-----AVSLSVTVVALGC-W 830
Qy 884 FIPKLHIWIARNIDIDPVIHSMGLKMECNTRRFVDDRRRELQYRVEVQNRVYKKEIQALD 943
Db 831 FTPKMYIIIA-----KPERNV-----847
Qy 944 AEIRKRLLESGLTITSTTSSSTSLLLGGGHLKPELIVTSGISOTPAASKNRTPSISG 10030
Db 848 -----SAFTTSVVRMHVGDGKL-----PCRS-----869
Qy 1004 ILPNLLSVLPVPIPRASWPFAEVMQIPMRRSVTFASQPQLEEACLPADQLINLRLA-HQ 1062
Db 870 ---NTFLNIFRRKKPGAGNANSN-----GKSVSW-SEFGGRQA--PKGQHWQRLSVHV 917
Qy 1063 QATEA---KTGLINLRIGIFSRITSSNKGSTASLADQKGLKAFAKSHMGLFTRLIPSSQT 1119
Db 918 KTNETACNQTAIVKPL-----TKSVQSGSKL-----TFSD 948
Qy 1120 ASCNAIYNPNODISPEASHPGNHLKPIHRGSLTKSGTHL-DHLTKD--PNELPIPT 1176
Db 949 ASTYTLINVEEDNTPSAHFSSPSSSVVHRRGPPVATPPPLPHLTAETPLFLASV 1008
Qy 1177 ISGG-----EQGDQTLLGGRYVKLLETKVNFQLPSNRPSVYQQPPSLRVRVG 1224
Db 1009 IPKGLPPLPQQQPQ-----QPPQPP-----QQPKSLMDQLQG 1043

RESULT 13
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor
A:Reference number: A42916; MUID:92317054
A:Accession: A42916
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <AB>
A:Cross-references: GB:D10891; NID:9220813; PIDN:BA01711.1; PID:d1002186;
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIPI:107750)
;Keywords: G protein-coupled receptor; transmembrane protein

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Query Match 3.8%; Score 256; DB 2; Length 1171;
Best Local Similarity 19.6%; Pred. NO. 2.le-09;
Matches 247; Conservative 180; Mismatches 513; Indels 322; Gaps 54;

Qy	137	SRRMSPAEMQRNHGKIIVLLGFELSTSRGPRD-----GLSELGAATMAV	182
Db	23	SERRV-----VAHMPGDIIGALF--SVHHQPTDVKVHERKCGAVRQYGIQRVEAMLHTL	76
Qy	183	EHINR-KELLPGYILEVTNDTQCDDPGVGVDYRFFHAIY-----	220
Db	77	ERINSDPTLLNITLTCGEIRDSCWHSAVALEQSTIEFTRDSLISEEEGLVRCVCGSSSF	136
Qy	221	QPSYRWVNLGLGASCEVYTESLAKVPYWNIVQVSFGSTSPALSDRREFFVPFYRTVAPDSS	280
Db	137	RSKKPIGVIGPGSSVAIQVNLQLFNIPQIAYSATSMDLSDKTLFKYFMVRVPSDAQ	196
Qy	281	HNPIARIAIRKFGMGVTVTFSSQNEEVHSLVANVNLVTELEAANTSCAATTIFAATDPKEOL	340
Db	197	QARAMVDIVKRYNW--TVYSAVHTCEGTCESGMEAFKDMSAKEGICIAHSYKIYSNAGEQS	255
Qy	341	L--LLRETDTRI---IIGSPSQELAQIILCEAYRLRMFGADYAWILLHESMGAPWMPDQR	394
Db	256	FDKLLKLRSLHLPKARVVACCEGVTVRGLLMA--MRRILGLAGEFLL---LGSDGWADRY	310
Qy	395	TACSNHIELQLAVENLIVVSTHNSIVGNVSY-----SGLNN-----HMFNSQLRQK	440

QY 608 RV---FKLRVATIAPLAFYTIIATFLSSVGALAIITFLAFLNHLRPERKLAIKLSPPKLSNIT 663
DB :
DB 560 RTGCEIIPPEVVSWTSFGHILALVAVGTIISWATLAVFLRHNSPVVKSTRELSEYII 619
QY 664 AVGCIFYVATVILLGLDHSITLPSAEDESFATVCTARVLLSAGSLAFSGFMAFTRVHRH 723
DB :
DB 620 LSGIVACYAVSFALLATPST-----TSCFTFRVIPPIAFVAVYSALLTKTNRIARI 670
QY 724 FTRTGS-----VFKDQMLODIQLLVGLGILLDALVLTLMWVTDPMERHLNHLLEISA 778
DB :
DB 671 L--AGSKRIILTKEPRELTFESQVVIWILVAQCIVGVGLMRD-----WPDATYAKYA 723
QY 779 TDRSVVYQPOVEVCRSOHTOMLSVLAYKGLLLVGVVYAMETRVHKIPALNDQQYIGV 838
DB :
DB 724 LPRKLILECDTE-----TKSFL-IPFEWFDFLIITCLTYAFKTRNLPL-ENFNKAFFGF 775
QY 839 SVYS-----VVITSVVVLANLISERVTLAFI-----TITALIILT-----S 875
DB :
DB 776 TISOPAKSLPFQKEHVIIIFQYCTVV-----VMIAFLVLHMGTTHKALVMSFSYSIS 827
QY 876 TTATLCILFIPLKHDINARNDDIDPVIHSMGLMECNTRRFVVDDRRLQRYVEQNRRVY 935
DB :
DB 828 ASVALALLFPFKLXII-----LMHP-----EKNIK-----ASYTTTKLIRCH 864
QY 936 KKEIQALDAEIRKLERLLESGLTTTSTTT-----SSSTSLLTGCGHLKP---ELTVTSGIS 988
DB :
DB 865 FGNSQAAYDSTSKOOHL---GSKTTARTSVQSGASKSXSMGGVTRTASVHVPVSRGST 921
QY 989 QTPAAKNRPSPISGIILPNLLLSVL-----PPVIPRASWPESAEMYQIPMRRSVTFASQPOL 1044
DB :
DB 922 HSTDVSTQTEGLSIPIPLMKFIVLNFDILLAASKRSRSFIVGRKKGLDDVDQOL 981
QY 1045 EEACLPADQ-LINURLAH--QOATEAKTGLI-----NRLRGIFSRTTSSNRK----- 1088
DB :
DB 982 VDACCRRYODEKINSSAANLLEESEDEVGALLADSIENSMTVLVS--TVAGRNVPLVPM 1033
QY 1089 -----STASLADQKGKAAFKSHMGL-----FTRLIPSSQTASHCAINIYN 1122
DB :
DB 1040 VPMIPVVTPLTAPSQEONDFEQAGEKCKQLCSKLSRKSPKQFLVHAPKRCSTSRV--- 1099
QY 1129 PNODSPISEASSHP--NGNHCLKPHIRGSLKFSG-----THLDHLTKDPNFLPTPTS 1178
DB :
DB 1097 -----SSYTIMSGNQILMSPMGVSSSAGSGSPSPMSFDFHLSDE----ELAQIS 1144
QY 1179 GGEQGDTLG-----GKYVYLKETKYNFQLPSNNRPSVVQ-QPPSL 1218
DB :
DB 1143 VRQLNQKLMGDNRVVMQWKRRRTLKNRGYALNCRRARRVNNQVQLEADNMMLRNQIKTL 1204
QY 1219 RERVEGS-----PRF-----PHRLIPTCISLSALAESEDRPGDSTS 1254
DB :
DB 1203 REALSEAQRMLHYEPFYQAYPSIVPSTTSPVTSLPTIARPIPVPPOSTA 1254

RESULT 12

A41939

G protein-coupled glutamate receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A41939; S15362
R:Houamed, K.M.; Kulijer, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.
Science 252, 1318-1321, 1991
A>Title: Cloning, expression, and gene structure of a G protein-coupled glu
A:Reference number: A41939; MUID:92022526
A:Accession: A41939
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1199 <MOD>
A:Cross-references: GB:M61099; NID:g397806; PIDN:AAAL19497.1; PID:g204460
A:Experimental source: cerebellum
A>Note: sequence extracted from NCBI backbone (NCBIP:60785)
R:Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.

RESULT 11

T21340
hypothetical protein F45H11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T21340; T2252
R:McMurray, A.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19409
A:Accession: T21340
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1267 <W1>
A:Cross-references: EMBL:Z78418; PIDN:CAB01699.1; GSPDB:GN00019; CESP:F45H11.4
A:Experimental source: clone F25D7
R:Kelly, P.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19537
A:Accession: T2252
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1267 <W12>
A:Cross-references: EMBL:Z78420; PIDN:CAB01711.1; GSPDB:GN00019; CESP:F45H11.4
A:Experimental source: clone F45H11
C:Genetics:
A:Gene: CESP:F45H11.4
A:Map position: 1
A:Introns: 38/3; 90/2; 149/3; 207/1; 356/2; 413/2; 458/2; 520/3; 691/3; 777/2; 796/2; 891/3

Query Match 4.2%; Score 283.5; DB 2; Length 1267;
Best Local Similarity 19.9%; Pred. No. 2.8e-11;
Matches 273; Conservative 198; Mismatches 508; Indels 393; Gaps 64;

QY 136 ESERMSPAEMORNHGKIVLLGLFEL-----STS RGP--RPDGLSELCAATMAVEHINR 187
Db | | | | | | | | | | | | | | | | | | | | | : | : |
23 QQSARMLVAEI---HG EIQIGALFPPIHQIQTSGESCGEIQEWGYGIQRSEIAMLTVKQLNE 79
QY 188 KRLPGYTLELVNDT-----QCD----PGVGVDRFFHAITYTPS 223
Db | | | | | | | | | | | | | | | | | | | | | : | : |
80 E--LP-FKLGLSTRDCSWTERIAEQTI AFLREGVAQCSCQTGCG-----NKKS 126
QY 224 TRMVVLGSACSEVTESLAKVVPWNIVQVSFGSTPALS DRPFYPFYRTVAPDS SHNP 283
Db | | | | | | | | | | | | | | | | | | | | | : | : |
127 VPVAVIGPKSSSTTAVQNLLQVFRIPQVGYSATTPOLSKREQGYFLRVPSDVFOAQ 186
QY 284 ARIAFIRKEGWGTVTTF SQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKEOLL L 343
Db | | | | | | | | | | | | | | | | | | | | | : | : |
187 AINLLHHVNTVVAVLYSAGNYGEKGFE SL--EKLIARS SSVCIAYSE---KITLAS 241
QY 344 RETDTRIIGFSQELAPQTL--CEAYRLRMFG-----AD-----YAMILHESMGA 387
Db | | | | | | | | | | | | | | | | | | | | | : | : |
242 EQEYRQVLT RLDSQNSRPPVVCFCGASRMFFKAQKHLADGKMOMKR FOWI-----GS 296
QY 388 PWMPOQTACS NHELQAVENLIVVSTH- NSIVGNNVSYSGLN--NHMFNSQLR-----K 439
Db | | | | | | | | | | | | | | | | | | | | | : | : |
297 DGWADRNDVV--EDLEEAGCSFIRIHAKIPGRQYYTALHPENNTHMPNRF EFWOOK 354
QY 440 QSAQFHGDGFGSGYGPRISAATQSDSRRRRRRGVVGTS GGHLFPEAISQY-----APQ 494
Db | | | | | | | | | | | | | | | | | | | | | : | : |
355 FNCQF-----AVSKED---KNENIRICSGDENLDE---QYKDPKLSQ 392
QY 495 TYDAWATALRALAA--EEHWRREEQSKLDGF D YTRSDMAWEFLOQMGL---HFLGVSG 550
Db | | | | | | | | | | | | | | | | | | | | | : | : |
393 VINSIRVVALIKAM YQDCRON-----STLCETMLSRNGTLLIYEYL NVTY 439
QY 551 PVSFSGP---DRWG-TTA FYOI-----QRGLLEPV-----ALV 579
Db | | | | | | | | | | | | | | | | | | | | | : | : |
440 SDQFKQPYVFD RGGDPAPWDILNI GTKDLDNPNYEVG SFKSI NDYGV EELDMTAKSMF 499
QY 580 YPATDALD-----FRCPRCRPVKWHS-----GQVPIAK 607
Db | | | | | | | | | | | | | | | | | | | | | : | : |


```
C:Genetics:
A:Gene: mGluR3
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-679/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>
F:577-599/Domain: transmembrane #status predicted <TM1>
F:614-634/Domain: transmembrane #status predicted <TM2>
F:646-664/Domain: transmembrane #status predicted <TM3>
F:689-709/Domain: transmembrane #status predicted <TM4>
F:735-756/Domain: transmembrane #status predicted <TM5>
F:770-791/Domain: transmembrane #status predicted <TM6>
F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match          5.0%; Score 336; DB 2; Length 879;
Best Local Similarity 20.1%; Bred. No. 3.2e-15;
Matches 199; Conservative 133; Mismatches 330; Indels 326; Gaps 45;

QY 151 GKVLVLGLFELSTYS-----RGRPPD-GLSELGAATMAVEHINRKR-LLPG-----YTL 196
DB 37 GDLVLGGLFPINEKGTGTECRGINEDRGIQRLKLEAMLFDAIDKNDVLLPGVKGVLGHIL 96
QY 197 ELVTNDT-----QCDDPGVGVDRFFHAIYTOPSTFRWMLLSGAC 234
DB 97 DTCSDRTYALEQSLFVFRASLTQVDEAYMCPDG-----SYAQENIPLLIAGVIGGS 150
QY 235 SEYTESLAKVVPYNNIVQVSGSTSPALSDRRPEFYRTVAPDSSHNPARIATIRKFGW 294
DB 151 SSVSIQVANLLRFLQPOISYASTSAKLSKSDYDARTVPPDFYQAKAMAEILRFNW 210
QY 295 GTVTTFSQNEEVSGLAVNNILVTELEANISCAATITFAATDFKQL-----LLRETDTTR 349
DB 211 TVYTSVASEGDYGETGTEAPEQEARLNICIAATAEKVGRSNIRKSYDSVIRELLQKPNAR 270
QY 350 IIGTSFQELAPQILCEAYRLRMFGADYAMILLHESMCA----- 387
DB 271 VVFLMRSDDSLRLIAAASRV-----NASFTWASDQWGAQESIVKGSBHVAYGATLLELAS 327
QY 388 -----PWMPD---QRTACS-----NH-----ELQLAVE----- 407
DB 328 HPVRFQDRFYQSLNPNYNNHNPFWRFEWQKFCQSLQNRKRNHRQICDKHLAIDSNVEQE 387
QY 408 -----NLIVVSTH-----NSIVGNVSYGLNNHMFNSQLRKQ-----SAQPHGQ 447
DB 388 SKIMFVNAVYAMAHALHKMQRTLCPNNTKLCDAKMLDKGLKYKDYLLKINFAPENPN 447
QY 448 DG-----FGSGYGPRIASIAATQSDSRRRRRGVVGTSGGHLFPALISQYAPQYDA 498
DB 448 KGADSIKFTDYGDGMG-RYNVFNQIHGKYSYLKV-----GH----- 485
QY 499 VMAIALALRAAEHWRNEBQSKLDGFDYTRSDMAWEFLQMGKHLFLGVSGPVSFSGPD 558
DB 486 -WAETLYLDVDSLHNSRN----- 511
QY 559 RVGTTFAYQIQRG-----LLEPVLYYPAPDALDFRQPCRPVKWH-----SGQVPIAKRV 609
DB 512 PCAPNEMKNMQPGDVCWCWICPCEPEYELVD--EFTCMDCGPGWPTADLSGCYNLPEDY 569
QY 610 FKLKVA-TTAPLAFYIATLSSVIGIALAIT-FLAFNLHFRKLKAIKLSKPSKLSNITAVGC 667
DB 570 IRWEDAAGIPV---TTACLGFMCTCIVITVF1KHN-----NTPLVKASGRELCYILLFGV 622
QY 668 IFYATVILLGLDHS1LPSAEDSFATVCTARVYLLSAGFSLATGSMFAKTVRYHRIF--T 725
DB 623 SLSYCMTFFF-----IAKPS-----PVICALRLGLGTSFAICYALSALTUKTNCIARIFDG 673
QY 726 RTGSEVFKRMQLQDIQLLVGLGLLVDALVTLWVYTDPMERHLNHLTLEISATDRSVVY 785
DB 674 KNGAQ-RPFISPSQVFC1GLILQIVMVSVWLI-----LETPGTRRYTLP 720
QY 786 PQQVEV---CRSQTHTWLSVLYAYKGLLVGVGYMAWETHRVKIPA-LNDSQIGVGSVY 841
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DB 721 EKRETVILKCNVKDSSMLISL--TYDVVLVILCTVYAFKTR--KCPENFNEAKFIGFTMY 776
QY 842 SVVITSAIVVLANLISERVTLAFITITALILTST-----TATLCL-----LF 884
DB 777 TTCTI-----IWLAF1PI--FYVTSDDYRVQVTTMCISVLSGSLGVVGLCLF 819
QY 885 IPKLHDIWARNDIIDPVTHSMGLKMECNTRFRVVDRELOLYRVEVQNRVYKKEIQALDA 944
DB 820 APKVHIV-----LFQP-----QKNV-VTHRLH----- 840
QY 945 EIRKLERLLESLTSTTTSTTSSTSLTT 972
DB 841 ----LNRFSVSGTATYSSQSSASTVYPT 864

RESULT 9
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000
C:Accession: JH0563; I58149
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Molecule type: mRNA
A:Experimental source: brain
R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venezia, D.; Haldeman, B.A.; McGrane,
Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to
A:Reference number: I58149; MUID:93332699
A:Accession: I58149
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-123; R, 125-912 <RES>
A:Cross-references: GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401
C:Comment: This protein is coupled to a G protein and evokes a variety of functions b
C:Genetics:
A:Gene: GLUR4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
F:588-610/Domain: transmembrane #status predicted <TRI>
F:625-645/Domain: transmembrane #status predicted <TII>
F:657-675/Domain: transmembrane #status predicted <III>
F:700-720/Domain: transmembrane #status predicted <TIV>
F:751-772/Domain: transmembrane #status predicted <TRV>
F:786-807/Domain: transmembrane #status predicted <TVI>
F:823-847/Domain: transmembrane #status predicted <VII>
F:98,301,454,484,569/Binding site: carboxylate (Asn) (covalent) #status predicted
F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match          5.0%; Score 336; DB 2; Length 912;
Best Local Similarity 22.1%; Bred. No. 3.4e-15;
Matches 193; Conservative 134; Mismatches 346; Indels 200; Gaps 36;

QY 148 RNHGKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLLPGYTLE 197
DB 44 RIDGDITLGLFPVH-GRGSEKACGKELKKEGIHRLKLEAMLFALDRINDDPDLNPNITLG 102
QY 198 LVTNDTQCDPGVGVDRFFHA----- 230
DB 103 ARILDT-----CSRDTHALEQSLTFYQALIEKDGTVEVRGSGGPPITTRPE-RVVGVI 154
QY 231 GSACSEVTESLAKVVPYNNIVQVSGSTSPALSDRRPEFYRTVAPDSSHNPARIATIR 290
DB 155 GASGSSIVMIVANILRLKFIQISYASTAPDLSNRSYDFSRVPSDYQAAQVMDIVR 214
QY 291 KFGWGTVTTFSSQNEEVSGLAVNNILVTE-LEANISCAATITP-----AATDFKQLLLRE 345
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C;Superfamily: metabotropic glutamate receptor 4
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F;568-590/Domain: transmembrane #status predicted <TRI>
F;605-625/Domain: transmembrane #status predicted <TII>
F;637-655/Domain: transmembrane #status predicted <III>
F;680-700/Domain: transmembrane #status predicted <TIV>
F;726-747/Domain: transmembrane #status predicted <TRV>
F;761-782/Domain: transmembrane #status predicted <TVI>
F;795-819/Domain: transmembrane #status predicted <VII>
F;203,286,338,402,547/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F;832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	5.1%	Score 343 5:	DB 2:	Length 872;
Best Local Similarity	21.6%;	Pred. No. 9.5e-16;		
Matches 191;	Conservative 115;	Mismatches 338;	Indels 241;	Gaps 36;
Qy 151	GRKVLGLGFELSTSRGPRD-----GLSELGAATMAVEHINR-KRLPG-----	193		
Db 30	GDVLGGFLPVHKQGPAAECGPNVHRGQIRLEAMLFALDRINRDPHLLPGVRLGAHIL 89			
Qy 194	-----YTLELVNTDTCQDGVGVDRFFH-----AIYQTPSTRMVMLLGSACSEVTE 239			
Db 90	DCSKSDTHAEQALDFVRASLRSGADGSRHICPDGSIATSDAPTAVTGVIGGYSDDVSI 149			
Qy 240	SLAKVVPYNNIVQVSGTSPALSDRREFPYFYRTVAPDSSHNPARIAFIRFGWGTVTT 299			
Db 150	QVANLLRLFOIPQISYASTSAKSDSKRYDYFARTVPDPFOAKAMAEILIRFNWTVYST 209			
Qy 300	FSONEEVHSLAVNNLVTELEAANISCAATI-----TFAATDFKEQL-LLLRDTDRRIIG 353			
Db 210	VASEGDYGETGIEAFEELEARNI-CVATSEKVGAMSRAAFGVVVRLQRPASRAVVL 268			
Qy 354	SFSQELAPOILCPAYRLRMFGADYAWILHESMGA-----	387		
Db 269	FTRSEDARELLAATQRL---NASFTWASDQGALESVVAGSERAEGAITTELASYPIS 325			
Qy 388	-----PW-----WPDORTACSNHELQLAIVENLIV-----	412		
Db 326	DPASYFQSLDPWNNSRNPNFREFW-EEEFHC-SFRORDCAAHSLRAVPFQESKIMFVWNA 384			
Qy 413	-----STHNSIVGNVNSYSGLNNHMFNSQL-----RKOSAQFHGDGFGGSGYGPRI 459			
Db 385	VYAMAHALHNMHPCPN-----TTHLCDAMPVNGRRLYKDFLVNVKFDAPFRP--- 434			
Qy 460	IAATQSDSRRRRRRGVVGTSGGHFLPEAISQYAPOTYDAVMAIALARAAEEHRRNEEQ 519			
Db 435	-ADTDDEVRFDR-----FGDGIGRYNIFTY-----LAGSGRYRYOKVG 472			
Qy 520	SKLDGFDYTRSDMAWEFLQMGKHLFLGVSGVPVSFG-----PDRVGTATFYQIORGLL 573			
Db 473	YWAEGTLTDSFIPWASPS-----AGPLPASRCSEPCQLQNEVKSVPQGEVCWCILC 522			
Qy 574	EPVALYYPATDALDFRCRCRPVKWH-----SGQVPIAKRVFKLRVA-TIAPLAFYTIATL 628			
Db 523	IPCQPYEYRLD-EFTCADCGLGWPNASLTGCPELPQEIYRWGDAAWAGCPV---TIACL 577			
Qy 629	SSVGIALATTF-LAFNLHFRKRLKAIKLSSPKLSNITAVGCIFVYATVILGLDHSHTLPSA 687			
Db 578	G-----ALATFLVLGVFVRHNATPVWKASGRELCVILLGGVFLCYCMTFVFIAPKPSI--- 629			
Qy 688	EDSFATVCTARVYLLSAGSLAFSGMFAKYRVIRIF---TRTGSVFKDKMLQDIQILLV 745			
Db 630	-----AVCTLRLGLGLTAFCVCSYALLTKTNRIARIFGGAREGAO-RPRFISPASOVAIC 683			
Qy 746	GGLLLVALLVTLWVYDTPMERHLNLTLEISATDRSVV-YQPOVEVCRSOHTQWLSQL 804			
Db 684	LALISGOLLIVAANLV-----VEAPGGKETAPERREVVTLRCNDRASMLGS 731			
Qy 805	YAYGILLLVGVYMWAMETRHVKIPA-LNDISOIGVSVSVITSVAIVVLANLISERVTL 863			

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Db      732 LAYNVLIIALCTLYAFKTR--KCPENFENAKFIQFTMYTTCI-----IWL 774
      864 AFITITALTITST-----TATLCL-----LFIPKLRHDI 891
Db      775 AFLPTI--FVFTSDRVQVTTMCVSVLSGSSVVLGCLFAPKLRHII 817

RESULT      6
JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C:Accession: JH0562
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of f
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; trans
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F:577-599/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TII>
F:646-664/Domain: transmembrane #status predicted <III>
F:686-709/Domain: transmembrane #status predicted <TIV>
F:735-756/Domain: transmembrane #status predicted <TRV>
F:770-791/Domain: transmembrane #status predicted <TVI>
F:804-828/Domain: transmembrane #status predicted <VII>
F:209,232,414,439/Binding site: carbohydrate (Asn) (covalent) #status predi
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

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Query Match	5.1%	Score 343;	DB 2;	Length 879;
Best Local Similarity	20.1%;	Pred. No. 1e-15;		
Matches	200;	Conservative 132;	Mismatches 323;	Indels 340; Gaps 45;
Qy	151	GTKIVLLGLFELS-----TSRGRPRDGLSELGAATMAVEHINRKR-LLPG-----YTL	196	
Db	37	GDVLGGFLPINEKGTGTECGRINEDRGIQRLFAMFLAIDEINKONYLLPGVKLGVLH	96	
Qy	197	ELVINDT-----OCDPGVGDVRFHFHAYITQPSRVMVLLGSAC	234	
Db	97	DTCSRDTYALBQSLEFVRASLTUKVDEAYMCPDG-----SYAQENIPLLIAGVIGGSY	150	
Qy	235	SEVTESLAKVPVYWNIVQVSGTSPALSORREPPYFRTVAPDSSHNPARIAIRKFGW	294	
Db	151	SSVSIQVANLLRFQIPQISVASTSAKLSKRSYDIARTVPPDYQAKAMAEILRFFNW	210	
Qy	295	GTVTTFSONEEVHSLVANVNLVTELEAANISCAATITFAATDFEQL-----LLLR	349	
Db	211	TYVSTVASEGDYGETGEAFQEARLNICATAEKVGRSNIRKSYDSVIRELLQKPNAR	270	
Qy	350	IIIGSFQSOELAPQILCEAYRLRWFAGDYAMILLHESMCA-----	387	
Db	271	VVVLFMRSDDSRRELIAANRV---NASFTVWSDGWGAQESIVKSGSEHVAYGAILLELAS	327	
Qy	388	-----PWMPD---ORTACS-----NH-----ELOLAVE-----	407	
Db	328	HPVQFDRIYFOSLNPYNHNRHPFRDWEQKFOCSLQNKNNHROVCDKHLAIDSSNVEQE	387	
Qy	408	-----NLIVVSTH-----NSTVGNVSYSGLNHHMFSQLRKQ-----SAOFHQ	447	
Db	388	SKIMFVNVAVMAHALHKMORTLCPTWTKLCDAMKILDGKKLYKEVLLKINTAFENPN	447	
Qy	448	DG-----FGSGYGPRIASATQSDSRRRRRRGVVGTSG-----GHLFPEAISQY	491	
Db	448	KGADSIKFDTFDGGMG-RYNVFNLOO-----TGGKVSYLKVGH-----	485	

Db	371	DDSTRKCTG-----	-----BERTGQDSAYEBQKGVQFVD	AVTAIAHALUHSWHQALCPGH	420
Qy	512	-----	-----HWRR-----	-----NEEQSKLGDGY-----	527
Db	421	TGLCPAMEPTDGR	TLHHYIRAVR	FNGSAGTPVMFENENGDPAGRYDIFQYQATNGSSASSGG	480
Qy	528	-----	-----TRSDMAWEFLQOMCKLHFLG	VSQPSFSGPDRVCGITAFYQIORGLLEPVA	577
Db	481	YQAVGQWAEALRUDM	-----EVLURWSGD	PHVEV-----PPSOCSLP-----CGPGERKKMYKGV-----PCC	531
Qy	578	LYYPATDAL-----	DFRCPRC-----	RPVKWHSQGVPIAKRVRKFLVATIAPIAFVYTIATL	628
Db	532	WHCEACDGYRFQWDE	FTCEACPGDMRPTNHT	CRCTP-----VVRLTSSPPAAALPL--LL	586
Qy	629	SSVGIALAITFLA	NLHFRKKAIAKUSPKLSNITAVGCI	FVVATVAVILLGLDHSHTLPSAE	688
Db	587	AVLGIMATTTIMATF	MNRHNDTPIVRASG	RELSVVLGTGFIYIAITFLM-----VA	637
Qy	689	DSFATVCTARVYLLS	AGSFLA	GSFMAKTVRVRIEFTR--TGSVEKDKMLQDLOILLVGG	747
Db	638	EPCAICAAERLLGL	GTILSYSALLTKNRYIEFQGRSVTPPPFISPT	SQLVITFG	697
Qy	748	LLLVDALLVTLWV	DDPMERHLNLTLEISATRS	VVYQPOVE--VCRSQHTQTWLSVLYA	806
Db	698	LTSLOVVGVIAWL	GAQPP-----HSV-----	IDYEBQRTVDPQARGVLKCDMSDLSLTGCLG	750
Qy	807	YKGLLLVVGVYMAWET	RHVXKIPALNDSOXIGVSVY	SV-VITSAIVVVLANLI--SERVTL	863
Db	751	YSLLLMWTCTVYIA	KARGVP--EFNEAKPIGFTWYTCIIWL	AFVPIFGTAQSAEKIYI	809
Qy	864	AFITITALITST	TATLCLFLP	KLHDI	891
Db	810	QTTTTLTVLSIL	SASVSGLMXYV	KPVTVI	837

RESULT 4
A49874
metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mGluR7
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A49874; 157954
R:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, T.
J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coupled to phospholipase C- β 1
A:Reference number: A49874; MUID:94117433
A:Accession: A49874
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:Cross-references: GB:D16817; NID:g458728; PIDN:BAA04092.1; PID:g458729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid receptor family
A:Reference number: 157954; MUID:94195260
A:Accession: 157954
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RE2>
A:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658
C:Genetics:
A:Gene: MGLUR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

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Query Match      5.2%; Score 348.5; DB 2; Length 915;
Best Local Similarity 20.4%; Pred. No. 4.6e-16;
Matches 17; Conservative 146; Mismatches 347; Indels 205; Gaps

Qy 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSELGAATMAVEHINR-KRLPPCYTL-196
Db 44 RIEGDVTLLGLFVPH-AKGPSVPCGDIKRENGHRLREAMLYALDOINSNPLLPNPTVLG-102

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Qy 197 -----ELVNDTQCDPGVGVDREFFHAIYIQPSTRMVMVLG 233
Db 103 ARILDGTSRDTYALEQLSTFYQALIQDRTSDVRCTNGE-----PPVFVKPE-KVGVGIG 155
Qy 232 SACSEVTESIAKVVPYNNIVQVSGTSPALSDRRPEFYFYRTVAPDSSHNPARAFIRK 291
Db 156 ASGSVSIMVANIIRLRFQIPOISTASTAPELSDRRYDFFSRVVPDPSFOAQMWDIVKA 215
Qy 292 FGWGTVTTFQNEEVHSLAVNNLTFLEAANI SCAATITFAATDFKEQL-----LL 343
Db 216 LGWNVYSTLASEGSGYEGKGVESFTQISKEAGGLCIAGSVRIPOERKDRITDFDRIIKQLL 275
Qy 344 RETDRIIGISFOBLAPQILCEAYRLRMFGADYAMILLHESMGAPWMPDORTACSNHELQ 403
Db 276 DTPNSRAVWIFANDEIKQILAAAKRADQVG-HFLMWGSDSMGSKTNP-----LHOHE 327
Qy 404 LAVENLIVSTHNSIVGNVSYSGLNHHMFPNSOLRQSOAQFHQDQFGSGYGPRIASIAAT 463
Db 328 DIAEGATIQPKRATV-----EGFDAYFTSRVLENNRRNRVFAEYWEENFNCKLTIGS 381
Qy 464 QSDSRRRRRGVGTSGGHLFPEAI-----SOYAPQ-----TYDAWAIALALRAAEHWR 515
Db 382 KKEDTRDKCTG-----QERIGKDSNYEQEGKVQFVIDAVYAMAHAL-----HHMK 427
Qy 516 N-----EEQSKDGFDTYRSDMAWEFLQMGKHLFLGVSG-PVSES-GPDRVGTTA 564
Db 428 DLCADYRGVCPMEQAGG-----KKLLKYIRHVNFGNSAGTVMFNKNGDAPGRYD 478
Qy 565 FYQIQ-----RGL-----572
Db 479 IFQYQTTNTNPGYRLIGQWTDLQNLIEDQMCKGVREITPSSVCTLPCKPGQKKTKQG 538
Qy 573 -----LEPVALYYPATDALDFRCPRC-----RPVKHSG--QVPIAKRVFKLKVATIAPL 620
Db 539 TPCCWTCPCDGYQYQFD--EMTQCHQCPYQRPNNRNTGQCNPIIKLEHSHSPWAVIP--594
Qy 621 AFYTIATLSSVGIATITFLAFNLHFKRAIKLSPKLSNITAVGCFYVATVILLGLD 680
Db 595 -----VFLAMIGIATIFVMAATFYINDTPIVRASGRELSVILLTGIFCYIITFLM--646
Qy 681 HSTLPSAEDSFATVCTARVYLLSAGSLAFSGMFAKTYRVHRIFTR--TGSVFMDKMLDII 739
Db 647 -----IAKPDVA-VCSFRRVFLGLGMCISYAALLTKTNRIYRIFEQGKSVTAPRLISPT 700
Qy 740 QLILVGLLIVDALLVTLVWVTPDPMERHUNLHNLTEISATDRSVVQPOVE--VCRSQHT 797
Db 701 SOLATSSLSISVQLLGVIFNFGVDP-----PNIIDY---DEHKTWNPEQARGVLKCDIT 752
Qy 798 QTWLSVLYAYKGLLVLVGVYMAWETRVHKVPALINDSOYIGVSVSV-VITSALVVVLANL 856
Db 753 DLQIICSLGYISLLMVTCTVYAIKTRGV-ENFNEAKPIGFTWYTCIWMFLAPIPIFFGT 811
Qy 857 I--SERVTAFITITALLTSTTATCLLFIPLKLDI 891
Db 812 AQSAEKLYIQTTTLTISMNLASVALGMLYMPKVYII 848
RESULT 5
JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1999
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002

RESULT 5
JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1999
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0561
A:Molecule type: mRNA
A:Residues: 1-872 <TAN>
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of

```
Db 346 PAVPVKNLRQDAIIIVGLFYETARKVCEVYKERLFGKKVYVWFLIGWADNWFKIYDP 405
Qy 394 RTACSNHELOLAVENLIVVSTHNSIVGNVNSYSGLNHMFNSQLRKOSAOFGHODGFGSG 453
Db 406 SINCTVDTEATEAVEGHITTEIVMLNPANTRISINMTSQEFVEKLTK----- 451
Qy 454 YGPRISIAATQSDRRRRRRGGVGTGGHLFPEAISQYAPQTYDAVWAIALALRAAEHW 513
Db 452 -----RLKRPETGG-----FOEAPLAYDAIWAIALALANKTSGGG 487
Qy 514 RRNEOSKLDGFDYTRSDMAWEFLQOMKGLHFLGVSPVSF-SGPDRTVGTTAFQIORGL 572
Db 488 GRS--GVRLEDNFYNNQITDQIYRAMSSSFEVSGVSHVVDASGRMAWTLIPQPGGS 545
Qy 573 LEPVALIYPATDALDPRPCRPVKNHSGQVPIAKRVKLRVATIAPIAYTTIATLSVG 632
Db 546 YRKIGYDSTKDDLSW----SKTDKWTGGSPADQTLIVKTRFRLSKLFTSVSVLSLG 601
Qy 633 IALAITFLAFNLHFRKLKAIKLSPLNSLTAVGCIFFVYATVILLGLDHTLPSAEDSFA 692
Db 602 IYLVAVCLSFNINSHVRVIONSOPNLNLTAVGCSALAAVPLGLDGYHI--GRNOFP 659
Qy 693 TVCTARVYLLSAGFSLAFGSMFAKTYRVHRIFTRTGSVFKD-----KMLQDIQIOLLVG 746
Db 660 FVQARLWLLGLGFSLYGYSMTFKIWWHTGFTK-----KEEKKEWKRTLEPHKLYATVG 714
Qy 747 GLLLDVALLVTVVDPMERHJLHNTLEISATDRSVVYQPOVEVCRSQHTQWLSVLYA 806
Db 715 LLVGMVLTALWIOIWDPLHRTTETAKPEKPIDVSIPLQLEHCSSRKMTWLGIFYG 774
Qy 807 YKGLLLVGVYMAWETHRVHKIPALNDSQYIGSVSVVITSVAIVVLANLISERVTLAFI 866
Db 775 YKGLLLGLIFLAYETKSVSTKINHRAVGMAYINAVLCLITAPVTMLSSQDDAFA 834
Qy 867 TITAILITTTATLCLLFIPLKLDIWARNDI IDPVTHSMGLKMECNTRRFVWDDERLQY 926
Db 835 FASLAIVFSSTYTLVFLVPKMRLLTRGEWQSEADQTMKTSSTN-----NNEEKS 888
Qy 927 RVEVONRVYKKEIQALDAIRKLERLLES 955
Db 889 LLEKENRELEKIIAEKEERVSELRHQLOS 917
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RESULT 2

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T29703
Hypothetical protein zk180.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29703
R:Pauley, A.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid zk180.
A:Reference number: 220669
A:Accession: T29703
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:U58748; PIDN:AAB52965.1; GSPDB:GN00022; CESP:zk180.1
A:Experimental source: strain Bristol N2; clone zk180
C:Genetics:
A:Gene: CESP:zk180.1
A:Map position: 4
A:Introns: 25/3; 98/2; 219/3; 253/3; 280/1; 309/1; 339/2; 357/3; 395/2
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Query Match 6.4%; Score 429.5; DB 2; Length 402;

Best Local Similarity 33.9%; Pred. No. 2.5e-22;

Matches 103; Conservative 60; Mismatches 104; Indels 37; Gaps 8;

Qy 535 EFLQOMKGLHFLGVSGPVSGFSDRTVGTTFAYQIORCLLEPVALIYPATDALDPRPCR 594

Db 11 KWEAIDNSSFOGLTGKRVFANNERLGLVDIKOWSDQGVYVFAVDGADD--EFKIIDST 68

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Qy 595 PVKWHSGOVPIAKRVKLRVATIAPIAFVYIATLSSVGIALAITFLAFNLHFRKLKAIKL 654
Db 69 TKGW---SPDDSTTERRREHIS-----SILFLAMSLF-----IKM 102
Qy 655 SSPKLSNITAVGCIFFVYATVILLGLDHTLPSAEDSFATVCTARVYLLSAGFSLAFGSMF 714
Db 103 SSPNLNIIAGSICTFASVIMGLD--TRIVSPDVFWLCTYKWTWLCIGTILSEGAMF 160
Qy 715 AKTYRVHRIFTRTGSVFKD-KMLQDIQIOLLVGGLLVDALLVTVVDPMERHJLHNT 773
Db 161 SKTRVHISFT---NIRMDRKAIKDKLFIILGILLFIDICVLVTFWAFVSPFS---YTVT 214
Qy 774 LEISATDRSVVYQPOVEVCRSQHTQWLSVLYAYKGLLLVGVYMAWETHRVHKIPALNDS 833
Db 215 ELPHIPEDNIVLIPEVEKCNSSHGVOAVLYAVXGVLMLGCLFALAWETHRVHNVNVPALNDS 274
Qy 834 QYIG 837
Db 275 KYIG 278
RESULT 3
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakani
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor
A:Reference number: A46742; MUID:93280152
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NAK>
A:Cross-references: GB:DJ13663; MID:g391856; PIDN:BAA03066.1; PID:g391857
A:Experimental source: retina
A>Note: sequence extracted from NCBI backbone (NCBI:133246, NCBI:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein
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Query Match 5.5%; Score 367; DB 2; Length 871;

Best Local Similarity 21.8%; Pred. No. 2.1e-17;

Matches 189; Conservative 130; Mismatches 361; Indels 188; Gaps 32;

Qy 151 GKIVLLGLFELSTSRG-----PRPDGLSELGAATWAVEHINR-KRLLPG----- 193

Db 31 GGLTLGGILFPVH-ARGAAGRACGALKKEQGVHRLEAMLYALDRVNADPELLFGVRLGARL 89

Qy 194 -----YTLLELVNTDQ-----CDPGVGVDFFHAIYTPQSTRMMLL 230

Db 90 LDTCSDTYALEQALSFVQALIRGRDGDGEASVRCPGV-----PPLRSAPERVAVV 143

Qy 231 GSACSEVTESTAKVYVYNNIVQVSGTSPALSDRRPEPFYFTRVAPDSSHNPARIATFR 290

Db 144 GASASSVIMVAVNLRLFAIPQISYASTAPELSDSTRYDFSRVPPDSYQAQAWDIVR 203

Qy 291 KFGWGTVTTFSSONEVHSLAVNNLV-TELEANISCAATITFAAT-----DFEQQLLLRL 345

Db 204 ALGNVYVSTLASEGNYGESGVEAFVQISREAGGVCAIOSIKIPREPKEGPHKVRRLME 263

Qy 346 TDTRIIGSFQSOELCAPOILCBAYRLRMFGADYAWILHESMGAPWWPDQRTACSNHELOLA 405

Db 264 TPNARGIILFANEDDIRRVLEATROANLTGHFLWVGSWSGSKISP-----ILNLE 314

Qy 406 VENLIVVSTHNSIVGNVNSYSGLNHMFNSQLRKOSAOFGHODGFGSGYPRISIAATQS 465

Db 315 EEAAGAI-----TILPKRASIDGFDQYFMTSRLENRRNIWFPAEFWEENFNCKLTSSGGS 370

Qy 466 DSRRRRRGVGTSGGHLFPFAISQ---YAPQ-----TYDAVWAIALALRAAE----- 511

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:06:10 ; Search time 41.85 Seconds
(without alignments)
2375.335 Million cell updates/sec

Title: US-09-715-962-6
Perfect score: 6705
Sequence: 1 MRIIPVQGYGPWPVAVL.....RLSLGDSBEEQQAPANGTE 1305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979.5	14.6	960	2 JE0356	gamma-aminobutyric
2	429.5	6.4	402	2 T29703	hypothetical prote
3	367	5.5	871	2 A46742	metabotropic gluta
4	348.5	5.2	915	2 A49874	metabotropic gluta
5	343.5	5.1	872	2 JH0561	metabotropic gluta
6	343	5.1	879	2 JH0562	metabotropic gluta
7	336.5	5.0	908	2 I49142	metabotropic gluta
8	336	5.0	879	2 JC7160	metabotropic gluta
9	336	5.0	912	2 JH0563	metabotropic gluta
10	306.5	4.6	999	2 T27628	hypothetical prote
11	283.5	4.2	1267	2 T21340	hypothetical prote
12	257.5	3.8	1199	2 A41939	G protein-coupled
13	256	3.8	1171	2 A42916	metabotropic gluta
14	240	3.6	1085	2 S40476	Ca(2+)-sensing rec
15	237	3.5	1078	2 A56715	calcium receptor (
16	233.5	3.5	1088	2 B56715	calcium receptor (
17	224	3.3	1218	2 S71376	glutamate receptor
18	223.5	3.3	1212	2 JC2131	metabotropic gluta
19	221.5	3.3	1079	2 I59362	calcium/polyvalent
20	220.5	3.3	1180	2 JC2132	metabotropic gluta
21	206	3.1	253	2 T29704	hypothetical prote
22	205.5	3.1	976	2 T51137	ionotropic glutama
23	203	3.0	962	2 D86186	hypothetical prote
24	200.5	3.0	941	2 T51135	ligand-gated chann
25	194.5	2.9	898	2 T05099	hypothetical prote
26	191.5	2.9	551	2 T30806	metabotropic gluta
27	180.5	2.7	953	2 E84732	probable ligand-ga
28	179	2.7	920	2 B84640	probable ligand-ga
29	178.5	2.7	1118	2 T27865	hypothetical prote

30 176.5 2.6 950 2 T51134 ionotropic glutama
31 167.5 2.5 934 2 T02742 probable ligand-ga
32 166.5 2.5 921 2 T51136 ionotropic glutama
33 166.5 2.5 923 2 F84732 probable ligand-ga
34 166.5 2.5 1047 1 OYRBR atrial natriuretic
35 166.5 2.5 1047 2 I45882 C-type natriuretic
36 166 2.5 1112 2 T28082 hypothethical prote
37 165.5 2.5 951 2 T51132 probable glutamate
38 164.5 2.5 925 2 T51133 ligand gated chann
39 164.5 2.5 975 2 A84550 probable ligand-ga
40 163 2.4 912 2 T51131 ligand gated chann
41 162.5 2.4 1047 1 OYHBR natriuretic peptid
42 160 2.4 847 2 T34577 probable export pr
43 160 2.4 925 2 T06128 hypothethical prote
44 155.5 2.3 938 2 T01809 hypothethical prote
45 155 2.3 454 2 S75741 hypothethical prote

RESULT 1
JE0356
gamma-aminobutyric acid receptor B precursor - human
N:Alternate names: GABA(B) receptor
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 12-Feb-1999
C:Accession: JE0356
R:Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante
Biochem. Biophys. Res. Commun. 250, 240-245, 1998
A:Title: GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine m
A:Reference number: JE0356; MUID:98440782
A:Accession: JE0356
A:Molecule type: mRNA
A:Residues: 1-960 <GRI>
A:Cross-references: GB:Y11044; NID:G2826760
A:Note: this ORF is not annotated in GenBank entry HSGTHLAL, release 109
C:Genetics:
A:Map position: 6p21.3-6p21.3
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:1-11/Domain: signal sequence #status predicted <Sig>
F:12-960/Product: gamma-aminobutyric acid receptor B #status predicted <MAT>
F:590-613/Domain: transmembrane #status predicted <TM1>
F:527-654/Domain: transmembrane #status predicted <TM2>
F:566-687/Domain: transmembrane #status predicted <TM3>
F:709-730/Domain: transmembrane #status predicted <TM4>
F:767-788/Domain: transmembrane #status predicted <TM5>
F:803-825/Domain: transmembrane #status predicted <TM6>
F:831-856/Domain: transmembrane #status predicted <TM7>
F:23,83,439,481,501,513,630/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 14.6%; Score 979.5; DB 2; Length 960;
Best Local Similarity 29.6%; Pred. No. 2.5e-60;
Matches 257; Conservative 155; Mismatches 364; Indels 93; Gaps 17;
QY 100 RLNSHNLPGSTNASHAHLLNLPQRQYLKVNQVFESRSPAEQNRHGKIVLLGLF 159
DB 129 RCDPDFHLVGSRSICSGQWSTP--KPHCQVNRTPHSRR-----AVYIGALF 175
QY 160 ELSTSRGPRPDGLSELCAATMAVEHINKR--LLPGYTELVNTQCDPGVGVDREFFHAI 218
DB 176 PMS---GGWPGGQACQPAVEMALADVNSRRDILPDYELKLIHDSKCDPGQATKLYELL 232
QY 219 YTOPSTRMWWLLSGSSEVTESLAKVVPYWNIVQVSGSTSPALSDRREFYFYFTVAPD 278
DB 233 YNDP---IKIILMPGCSVSVTLVAEARMNLIIVLSGSSSPALSNRQRFPTFFTHPSA 289
QY 279 SSINPARIPIRFQGWGTVTTFSSQNEVHSLAVNVLVTELEAANISCAATITFAATDEKE 338
DB 290 TLHNPTRVKLFKRWGKKIATIQQTTEVFTSLDDELRVKEAGIE---ITFRQSPFSD 345
QY 339 QLL---LLRETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWHP---DQ 393

ALIGNMENTS


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FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 893 908 TSSTKTYISYNSHSI -> SKSSVEFFPMVKSGSTS (IN ISOFORM B).
FT VARSPLIC 454 501 SAGTPVFNENGADPGRYDIFQYITNKSTKEYVIGHWTNO
LHLKVED -> CRGQIOMSLPWPITLTPSPSSSWAVALLS
LWKREMLDVMITSSSIK (IN ISOFORM C).
FT VARSPLIC 502 908 MISSING (IN ISOFORM C).
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 I -> N (IN REF. 1).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101740 MW; 95C2D5883DAF6FDE CRC64;

Query Match 5.0%; Score 337.5; DB 1; Length 908;
Best Local Similarity 20.7%; Pred. No. 1.2e-15;
Matches 207; Conservative 153; Mismatches 339; Indels 301; Gaps 46;

QY 146 MORNH-----GKIVLGLGFELST--SRG-----PRPDGLSELGAATMAVEHIN 186
DB 28 MORTHQEVAHSIRVDGDIILGLFPVHAKGERGVPCELGELKKEGIHRLAEMLYAIDQIN 87
QY 187 R-KRLLPGYTL-----ELVNDTQC---DPGCVGDRFFH 216
DB 88 KDPDLLSNTLTVRILDTCSRDTYALEQSLTFYQALIEKDASDKANGDP----- 138
QY 217 AIYTOPSTRMVMVLGSACSEVTESLAKVVPYWNIVOSFGSTSPALSDREEFPYFRTVA 276
DB 139 PIFTAPD-KISGVIGAAASVSIMVANIILFKIPIQISYASTAPELSDNTRIDFFFSRVP 197
QY 277 PDSSHNPARIAIRKFGWGTVTTFSON---EEVHSLAVNNLVTLEAANISCAATITFAA 333
DB 198 PDSYQAQAMVDIVTALGNWYVSTLASEGNYGESGVEAFTQISREIGVCVIAQSQKIPREP 257
QY 334 T--DFKEQLLLRET-DTRIIGSFQELAPQILCBAYRLRMFGADYAWITLHESMG---A 387
DB 258 RGEFEKTIKRLLETPNARAVIMFANEDIRIRLEAAKLNQSG-HFLWIGSDSWGSKIA 316
QY 388 PWWPDQRTACSNHQLAVENLIVSTHNSIVGNVNSYSGLNNH-----MENSQLRKQSA 442
DB 317 PVIQOEETA-----EGAV-----TILPKRASIDGDFRYFRSRTLANNRRNWF 360
QY 443 QPHGQDGFEC---SGYGPRIISAATQSDSRRRRRRGVGTSGGHLFPEAISQYAPQTYD 499
DB 361 EF-WEENFCCKLGSHGKRNSHIKKTGLERIARDSSEYQEGKVQF-----VIDAV 409
QY 500 WAIALALRAAEHWRNE-----BQSKLDGFDYTRSDMAWBEFLQOMKGLHFLGVS 549
DB 410 YSMAYAL-----HNMHKOLCPGYIGLCPRMSTIDG-----KELGVIKAVNENGA 455
QY 550 G-PVSFS-GPDRVGTAFQIQ-----RGLLEPV 578
DB 456 GTPVTFNENGADPGRYDIFQYITNKSTKEYVIGHWTNLHLKVEDQMAHREHTHPASV 515
QY 579 -----YYPATDALDERCPCO-----RP----- 595
DB 516 CSLPCKPGERKKTIVKGVPCWCWICERCEGNYQVDELS--CELCPDQRPNNMRTGCOLIP 573
QY 596 ---VKWHS--GOVPIAKRVFKLRVATPIAFYTTIATLSSVGIALAITFLAFNLHFRK 650
DB 574 IKLEWHSPWAVVPVAILGIIATTF-----VIVTFVRYN---DTP 612
QY 651 AIKLSPLKLSNTAVGCIFFYATVIVILLGDHSLPSAEDSFATVCTVARYVLLSAGFSLAF 710
DB 613 IVRASGRELSVLLAGIFLCYSITFL-----MIAAPDTI--ICSFRRVFLGLGMCFSY 663
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Search completed: April 30, 2002, 10:08:14
Job time: 201 sec

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QY 711 GSMFAKTYVRHRIFFR-TGSVFCKMQLQDIQLILLVGGLLLDALLYLWVWTD----- 764
DB 664 AALLTKTNRIHRIFFEQGKKSVTAPKFI SPASQLVITFSLISVQLLGVMFVVDPPHII 723
QY 765 -----MERHLNLTLEISATDRSVVYQPOVEVCBSQHTQTWLSVLVYAKGLLLVGVY 817
DB 724 DYGEQRTLDPEKARGVLKCDISDLSL-----ICS-----LGYSILLMVTCTV 765
QY 818 MAWETRHHVKIPALNDSQYIGSVSVY-VITSALVVVLANLI--SERVTLAFITITAILT 874
DB 766 YAKTRGVP-ETFNEAKPIGFTWYTCIILWLAIFIPIFFGTAQSAEKMYIQTITLTYSMSL 824
QY 875 STATLCLLFIPLKLDIWARNDIIDVHSMGLKMECNTRRFVVDRELOQYREV---- 930
DB 825 SASVSLGLMYMPKVYII-----IFHP-----BQNVQ-----KKRSFKAVVTAAT 864
QY 931 -QNRVYKKEIQALDAEIRKLERLLESGLTTTSTTSSSTS 969
DB 865 MOSKLIQKGNDRPNGEVK--SELCSLETNTSSTKTYIS 902
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Db 139 PIFTPD-KISGVICAAASSYIMVANILRLFKIPQISYASTAPELSDNTRDYFSRVVP 197
Qy 277 PDSHNPARIATIRKFGMTVTTSQNF---EEVHSLAVNNLVTELEAANISCAATITFAA 333
Db 198 PDSYQAQAMVDIVTALGNNVYSTLASEGNYGESGVEAFQTQISREISGVCVIAQSQKIPREP 257
Qy 334 T--DFKQLLLRLRET-DTRIIGSFQSLAPQICEAFLRMFGADYAWILHESMG---A 387
Db 258 RPGEFEKIIIRLLETPNARAVIMFANEDIRILEAAKLNQSG-HFLWIGSDSMGSKTA 316
Qy 388 PWNPDQRTACSNHELQALAVENLIVVSTHNSIVGNVYSGLNNH-----MENSQLRKQSA 442
Db 317 PVYQOEIA-----EGAV-----TILPKRASIDGDFRYFRSRTLANNRRNVWFA 360
Qy 443 QFHQDQFGF---SGYGPRIATAQSDRRRRRGVGTSGHGLFPEAISQYAPQTYDAV 499
Db 361 EF-WEENFGCKLGSGRNHHKCTGLERTARDSSYEQEGKVQF-----VIDAV 409
Qy 500 WATLALRAAEHWRNEEQSKLQDFDYTRSDMAW-----EFLQMGKHLFLGVSG-PVSVF 554
Db 410 YSMAYAL-----HNMHKERCPCYIGLCPRMVTIDGKELIGYTRAVNFGSAGTPVTF 461
Qy 555 S-GPDRTGTTAFYQIQ-----RGLLEPVAL-----578
Db 462 NENGDAFGRYDIFQIINKSTEYKIIQHTWNQLHLKVEDMQWANKRHTHPASVCSLPCK 521
Qy 579 -----YYPATDALDFRCPRC-----RP-----VKW 598
Db 522 PGERKKTGVKVPCCWHCEGCEGYNQVDELS--CELCPDQRPINRTCCQRIPIIKLEW 579
Qy 599 HS--GVQPIAKRVKPLRVATIAPIAFYTIATLSSVGIATITFLAFNLHFRKLKAIKLS 656
Db 580 HSPWAVVPVFTAILGIATTF-----VIVTFVRYN-----DTPIVRASG 618
Qy 657 PKLSNITAVGCIFFYATVILLGLDHSITLPSAEDSFATVCTARVYLLSAGFSIAFGSMFAK 716
Db 619 RELSVILTGFLCYSTFL-----MIAAPDTI--ICSFRIIFLGUMCFSYAALLTK 669
Qy 717 TYRVHRIFR-TGSVFKDKMLQDIQLILVGLLGLLDVALLVTLVWVTPDPMERHLNLTLE 775
Db 670 TNRIHRIFEQCKSWTAPKFISSPQSQVITFSLISVQLLVGVFVWVDPHP-----TII 723
Qy 776 ISATDRSVVYQPOVEKRSQHTQWLSVLYAYKGLLLVGVVYMAWETRHVKIPALNDSOY 835
Db 724 DYGEQRTLDPENARGVLKCDISLCSGLYSILLMTCTVYIAKTRGVP-ETENEAKP 782
Qy 836 IGVSVYSV-VITSAIVVVLNLI--SERVTLAFITILITLSTATLCLLFIPLKHLDIW 892
Db 783 IGFTMYTTCIILWAFIPIFFGTQAQAEKMYIQTTLTVSMLSUSASVSLGMLYMPKVYIII- 841
Qy 893 ARNDIIDPVIHSMGLKMECNTRRFVVDORRELQYRVEV-----QNRVYKKEIQALDAEIR 947
Db 842 -----IFHP-----EQNVQ-----KRRKSFRAVTAATMQSKLIQKGNDRPNGEVK 882
Qy 948 KLERLESGLTTTSTTTSSSTS 969
Db 883 --SELCSLETNTSSTKTYS 902

RESULT 15
MGR8_HUMAN
ID MGR8_HUMAN STANDARD; PRT; 908 AA.
AC 00222; 015493; 095945; 095946;
DT 01-NOV-1997 (Rel. 35, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN MGR8 OR GPRC1H OR MGLUR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rostock P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells."
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=97446143; PubMed=9299241;
RA Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;
RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT disproportionately large gene located at 7q31.3-q32.1."
RL Genomics 44:232-236(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RC TISSUE=Fetal brain;
RA Malherbe P., Kratzelisen C., Lundstrom K., Richards J.G., Faull R.L.M.,
RA Mutel V.;
RT "Cloning and functional expression of alternative spliced variants of
RT the human metabotropic glutamate receptor 8."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U92459; AAB51764.1; -
DR EMBL; U95025; AAB72040.1; -
DR EMBL; AJ236921; CAB36968.1; -
DR EMBL; AJ236922; CAB36969.1; -
DR GCRDB; GCR_1889; -
DR GCRDB; GCR_2604; -
DR MTM; 601116; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01058; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction; Alternative splicing.
FT SIGNAL 1
FT CHAIN 34 908
FT METABOTROPIC GLUTAMATE RECEPTOR 8.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 584 608
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 609 620
FT TRANSMEM 621 641
FT DOMAIN 642 647
FT TRANSMEM 648 668
FT DOMAIN 669 695
FT TRANSMEM 696 716
FT DOMAIN 717 746
FT TRANSMEM 747 768
FT TRANSMEM 769 781
FT TRANSMEM 782 803
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QY 350 IIGSFQELPOLCEAYRLRMFGADYAWILHESMCA----- 387
Db 271 VVVLFRMSDDRELIAANRV---NASFTWASDGGWAQESIVKSGSHVAYGATLLELAS 327
QY 388 -----PMWPD---ORTACS-----NH-----ELQLAVE----- 407
Db 328 HPVROFDYFQSLNPNYNNHNPWFDFWQKFOCSLONKNNHQQVCDKHLAIDSSNVEQE 387
QY 408 -----NLIVVSTH-----NSIVGNVSYSGLNHMFNSOLRKO-----SAQFHGQ 447
Db 388 SKIMEFVNNAVAMAHKMQRTLCPTTKLCDAMKILDGKLVKEYLLKINFETAPENPN 447
QY 448 DG-----FGSGVGPRISTAOTSRRRRRRGVGTSG-----GHLPEALISQY 491
Db 448 KGADSIKVEDTFCGDMG-RYNFENLQO-----TGGKYSYLVKVGH----- 485
QY 492 APQTYDAVMAIALARAEHEHRRNEEQSLDGFYTRSDMAWEFFLOQMKLHFLVSGP 551
Db 486 -----WAEFLSDVDVSIHSRN-----SVP 505
QY 552 VSFGSDPRVGTGTAFTYQIRG-----LLEPVLYYPATDALDFRCRCRPVKWH-----SGQ 602
Db 506 TS-QCSDPCAPNEMKNMQGDVCCWICICEPEVEYLVD--EFTCMDCGPGOWPTADLSGC 562
QY 603 VPIARVFKLRVA-TIAPLAFYTIATLSSVGIATIT-FLAFNLHFKKAKILSSPKLS 660
Db 563 YNLPEYIKWEDAWAIGPV---TIAGLGFCTCIVITVFIKHN-----NTPLVKASGRELC 615
QY 661 NITAVGCIPIVYATVILLGLDHSFLPSAEDSFATVCTARVLLSAGESLAFSGMFAKTVR 720
Db 616 YLLFGVLSYSCMTFFF-----TAKPS-----PVICALRLGLGTSFAICYSAALLTKTNCI 666
QY 721 HRIF---TRTSVFKDKMLQDIQILILVGGLLLDALLVTLWVYDPMERHLNLTLEISA 778
Db 667 ARIFDGVKNGAO-RPKFISPSQVFICGLLIVQIVMVSVWLI-----LETPG 713
QY 779 TDRSVYVQPOVEV---CRSQHTQTLWSVLYAYKGLLVGVYVMAWETRVHWKIPA-LNDSQ 834
Db 714 TRYTLPEKRETRVILKCNVKDSMLISL--TYDVLVILCTVYAFKTR--KCPENFNEAK 769
QY 835 YIGSVSYVWITSIVVLANLISERVTLAFITITILTST-----TATLCL----- 882
Db 770 FIFGTYMTTCI-----IWLAFLPI--FYVTSYDYRVOTTTMCISVSLSGF 812
QY 883 -----LFIPKLDHIWARNDIIDPVHSMGLKMECNTRRFVDDRELQYRVEVQNRVYKK 937
Db 813 VVLGCLFAPKVIH-----LFQP-----QKNV-VTHRLH-- 840
QY 938 ETQALDAEIRKLERLESGLTTTSTTSSSTSLLT 972
Db 841 -----LNRFSVSGTATTYSOSSASTYVPT 864

RESULT 14
MGR8_RAT ID MGR8_RAT STANDARD; PRT; 908 AA.
AC P70579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97168760; PubMed=9016353;
RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile.";
```

```

RL Mol. Pharmacol. 51:119-125(1997).
CC !- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC !- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION INCEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMMILLARY BODY.
CC !- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U63288; AAB09537.1; -
CC GCRDb; GCR_1411; -
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7cun3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01058; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family; Olfaction.
CC SIGNAL 1 33
CC CHAIN 34 908
CC DOMAIN 34 583
CC TRANSMEM 584 608
CC FT DOMAIN 609 620
CC TRANSMEM 621 641
CC FT DOMAIN 642 647
CC TRANSMEM 648 668
CC FT DOMAIN 669 695
CC TRANSMEM 696 716
CC FT DOMAIN 717 746
CC TRANSMEM 747 768
CC FT DOMAIN 769 781
CC TRANSMEM 782 803
CC FT DOMAIN 804 818
CC TRANSMEM 819 843
CC FT DOMAIN 844 908
CC FT CARBOHYD 95 95
CC FT CARBOHYD 298 298
CC FT CARBOHYD 452 452
CC FT CARBOHYD 480 480
CC FT CARBOHYD 565 565
CC SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;

Query Match 5.1%; Score 339.5; DB 1; Length 908;
Best Local Similarity 21.0%; Pred. No. 8.4e-16;
Matches 206; Conservative 154; Mismatches 357; Indels 265; Gaps 43;

QY 146 MQRNH-----GKIVLLGLFELST--SRG-----PRPDGLSELGAATMAVEHIN 186
Db 28 MORTHSQBYAHISIRVDGDIILGLLPVHAKGERGVPCGKELKKEGHIHRLAEMYAIDQIN 87
QY 187 R-KRLPGYTL-----ELVTNDTC-----DPGVGVDRFPH 216
Db 88 KDPDLLSNITLGVRLDTCSDRTYALEQSLTFVQALIEKDSADVKCANGDP----- 138
QY 217 AIYTOPSTRMVMLLGSACSEVTESLAKVVPYWNIVQVSGTSPLSDRREPFYRTVA 276
Db 217 AIYTOPSTRMVMLLGSACSEVTESLAKVVPYWNIVQVSGTSPLSDRREPFYRTVA 276
```

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Db 210 VASEGDVETGIEAFELARARNI-CVATSEKVGGRAMSRAAFEGVVRRALLQPSARVAVL 268
QY 354 SFSQELAPQIICEAYRLRMFGADYAWILHESMGA----- 387
Db 269 FTRSEDARELLAATLQRL---NASFTWASDGMGALESVVAGSERAAGAITTELASYPIS 325
QY 388 -----PW-----WPDQRTACSNHELQLAVENTLIV----- 412
Db 326 DFASYFOSLDPMNNSRPNWFREFW-EERFHCFSFRDCAAAHSLRAVPFPQESKIMFVNA 384
QY 413 -----STHNSITGVNVSYSGLNNHMFNSQL-----RKQSAQHGQDGFSGVGPRI 459
Db 385 VYMAHALHNNHRRALCPN-----TTHLCDAMRVPNGRRLLKDFVLNVKFDAPFRP--- 434
QY 460 IAATQSDSRRRRRRGVGTSGGHLFPPEALISQVAPOTYDAVMAIALARAAEEHWRNEEQ 519
Db 435 -ADTDDEVRFDR-----FGDGRYNYITY-----LRAGSRYRQKVG 472
QY 520 SKLDGFDYTRSDMAWEFLQOMKHLHFLGVGVPVSFG-----PDRVGTAFYQIQGLL 573
Db 473 YWAEGLTLDTSFIPWASPS-----AGPLPASRCSEPCLONEVKSVPQGEVCCWLC 522
QY 574 EPVALYYPATDALDPRCPRPVKWH-----SGQVPIAKRVFKLRA-TIAPLAFYTIATL 628
Db 523 IPCOPYEYRLD--EFTCADGLGVWPNASLTGCFELPQBYIRMGDAWAGPV---TIACL 577
QY 629 SSVGIALAITE-LAFNLHFRKAIKSLSPKLSNITAVGCIFFVYATVILLGLDHSHTLPSA 687
Db 578 G-----ALATFLVGVFVRHNATPVVKAAGRELKCYLLGGVFLCYCMTFVFIAPST--- 629
QY 688 EDSFATVCTARVYLLSAGFSLAFGSMFAKTYVRHIF--TRTGSVFKDKMLQDIQILIV 745
Db 630 -----AVCTLRRLGLGTAFSCVYCSALLTKTNRIARIFGGAREGAQ--RPRFISPASQVAIC 683
QY 746 GGLLVLDALLVTLVWVTDPMERHLNHLNLTLEISATDRSVV-YQPOVEVCRSHQTOHWLSVL 804
Db 684 LALLSGQLLVIAAMLV-----VEAPGTGKETAPERREVVVTLRCNHRDASMLGS 731
QY 805 YAYKGLLVGVWYMAWETRRHKIPKA-LNDSQVIGVSVSWITSAIVVVLANLISERVTL 863
Db 732 LAYNVLLIATLCTLYAFKTR--KCPENFNEAKFIGHTMYTTCI-----IWL 774
QY 864 AFITITAILLST-----TATLCL-----LFTPKLHDI 891
Db 775 AFLPI--FYVTSSDYRVQVTTMCSVSVSLSGSVVLGCLFAPKLHII 817

RESULT 13
MGR3_RAT
ID MGR3_RAT STANDARD: PRT: 879 AA.
AC P31422;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR GPRC1C OR MGLUR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT
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CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M92076; -; NOT_ANNOTATED_CDS.
CC PIR: JH0562; JH0562.
CC GCRDB: GCR_0362;
CC InterPro: IPR001828; ANF_receptor.
CC InterPro: IPR000337; GPCR_Mgr.
CC Pfam: PF00003; 7tm_3; 1.
CC PRINTS: PR001094; ANF_receptor; 1.
CC PRINTS: PR00248; GPCR_MGR.
CC PRINTS: PR01053; MTABOTROPIC3R.
CC PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE: PS00982; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 879 METABOTROPIC GLUTAMATE RECEPTOR 3.
CC DOMAIN 23 576 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 577 599 I (POTENTIAL).
CC DOMAIN 600 613 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 614 634 II (POTENTIAL).
CC DOMAIN 635 645 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 646 664 III (POTENTIAL).
CC DOMAIN 665 688 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 689 709 IV (POTENTIAL).
CC DOMAIN 710 734 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 735 756 V (POTENTIAL).
CC DOMAIN 757 769 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 770 792 VI (POTENTIAL).
CC DOMAIN 793 802 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 803 828 VII (POTENTIAL).
CC DOMAIN 829 879 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 439 439 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;

Query Match 5.1%; Score 343; DB 1; Length 879;
Best Local Similarity 20.1%; Pred. No. 4.5e-16;
Matches 200; Conservative 132; Mismatches 323; Indels 340; Gaps 45;

QY 151 GKIVLIGLIFELS-----TSRGRPDGLSELGAATWAVEHINRKR-LLPG-----YTL 196
Db 37 GDLVGLGLFPINEKGTGTGTECGRINEDRGIOKLEAMLFAIDKNDKLVLLPGVKVGVHLL 96
QY 197 ELVTNDT-----QCDPGVGVDVRFHAIYTPQSTRMVLGSGAC 234
Db 97 DTCSDRYALEQSLFVFRASLTKVDEAEYMCPDG-----SYAIOENPLLIAGVIGSY 150
QY 235 SEVTESLAKVYPYNNIVQVSGTSPALSDRREFFYFTVAPDSSHNPARTAFIRKFGW 294
Db 151 SSVSIQVANNLRLEIQIPQISYASTSAKLSKDSRYDYFARTVPDPFYQAKAMAEILRFENW 210
QY 295 GTVTFSSQNEEVHSLAVNNVLTELEAANISCAATTFPAATDFKEQL-----LLLRETDTR 349
Db 211 TVYSTVASEGDYGETGIEAFQEALRNICIAATAEKVGRSNIRKSYDSVIRELLQKPNAR 270
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QY 565 FYQIQ-----RGL-----572
Db 479 IFQIQTNTPNGYRLICQWDELOLNIEDMONGVGVRIPSSVCTLPCKGQRKTKQG 538
QY 573 -----LEPVAXYPATDALDFRCPRC--RPVKHSG--OVPIAKRVFKLRVATIAPL 620
Db 539 TPCWCWCEPCDGYOYQFD--EWTQCHCPYDQRPENRTCCQNIPIKLEWHSPWVIP--594
QY 621 AFYTIATLSSVGIAMAITFLAPNLHFRKLKATKSSPKLSNTATGVCIFYATPVILLGLD 680
Db 595 -----VFLAMGLIITIEFMATFIYNDTPIVRASGRELSVLLTGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFAKTYVHRIFTR--TGSVPKDKMLQDI 739
Db 647 -----IAKPDVA--VCSFRVFLGLGMCISYAALLKTRNIYRIFEGKKSVTAPRLISPT 700
QY 740 QLILVGLGLLDVALLVTLWVTPDMERHLHNLTLTLEISATDRSVVYQPOVE--VCRSQHT 797
Db 701 SOLAITSSLVOLLGVIFWGVDP-----PNIIDY---DEHKTWNPQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLVGVYMAWETRRHKIPALNDSOYIGVSYSV--VITSATVVVYLANL 856
Db 753 DLQICSLGYSILLMVTCTVYAIKTRGP--ENFNEAKPIGFTMYTTCIVWLAFIPIFFGT 811
QY 857 I--SERVTLAFTITALLITSTATLCLLFTPKLHDI 891
Db 812 AOSAELKLIQTTTLTISMNLSASVALGMLYMPKVYII 848

RESULT 11
MGR4_HUMAN STANDARD; PRT; 912 AA.
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=96346635; PubMed=8738157;
RA Makoff A., Lelchuk R., Oxer M., Harrington K., Emson P.;
RT "Molecular characterization and localization of human metabotropic
RL glutamate receptor type 4.";
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
[2]
SEQUENCE FROM N.A.
MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RL pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
[3]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=95342351; PubMed=7617140;
RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4.";
RL Neuropharmacology 34:149-155(1995).
RL
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
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```
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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QY 621 AFVTIATLSSVGLATLTTFLAENLHPKRLKAIKLSPKSLNITAVGCIFFVYATVILLGLD 680
 Db 595 -----VFLAWGLIATFVATIRINDTIVRASGRLSVLLTGILCYITFLM--- 646
 QY 681 HSTPLSAEDSFATVCTARVYLLSAGFSMFARKYRHRIFTR-TGSVFKDKMLQDI 739
 Db 647 -----IAKPDVA-VCSFRRVFLGLGMCISYAALLTKTNRIYRIFEQCKSVTPRLISPT 700
 QY 740 QILLVGGLLLVALLVTLVMTDPMERHUNLTLTSAIDRSVVYQPOVE--VCRSQHT 797
 Db 701 SOLAITSSISVOLLGVFIWFGVDP-----PNIIDY---DEHKTMPQEQARGVLKCDIT 752
 QY 798 QTWLSVLVYAKGLLVGVYVMAETHVKIPALNDQSYIGSVYVSV-VITSAIVVLANL 856
 Db 753 DLIQICSLGYSILLMTCTVYALKRGVP-ENENAKPIGTMTTTCIVMLAIPIFFGT 811
 QY 857 I--SERVTLAFITITALLTSTTATLCLLFPKLHDI 891
 Db 812 AQSAEKLYTQTTLTISMNLSASVALGMLYMPKVYII 848
 RESULT 10
 MGR7_RAT STANDARD; PRT; 915 AA.
 AC P35400;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
 GN GRM7 OR GPRC1G OR MGLUR7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94117433; PubMed=8288585;
 RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
 RA Mizuno N., Nakanishi S.;
 RT "Molecular characterization of a new metabotropic glutamate receptor
 RT mGluR7 coupled to inhibitory cyclic AMP signal transduction.";
 RL J. Biol. Chem. 269:1231-1236(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
 RX MEDLINE=941195360; PubMed=8145723;
 RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
 RA Westbrook G.L.;
 RT "Cloning and expression of a new member of the L-2-amino-4-
 RT phosphonobutyric acid-sensitive class of metabotropic glutamate
 RT receptors.";
 RL Mol. Pharmacol. 45:367-372(1994).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.

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 or send an email to license@sib-sib.ch).

 DR EMBL; D16B17; BAA04092.1; -;
 DR EMBL; U06832; AAA20655.1; -;
 DR GCRDb; GCR_0945; -;
 DR GCRDb; GCR_0946; -;

InterPro; IPR001828; ANF receptor.
 InterPro; IPR000337; GPCR_Mgr.
 Pfam; PF00003; 7Cm3; 1.
 Pfam; PF01094; ANF_receptor; 1.
 PRINTS; PR00248; GPCRMR.
 PRINTS; PR00593; MTABOTROPICR.
 PRINTS; PR01057; MTABOTROPCTR.
 PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 PROSITE; PS02529; G_PROTEIN_RECEP_F3_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 Multigene family; Olfaction.
 SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
 FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 591 615 I (POTENTIAL).
 FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 628 648 II (POTENTIAL).
 FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 655 675 III (POTENTIAL).
 FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 703 723 IV (POTENTIAL).
 FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 754 775 V (POTENTIAL).
 FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 789 810 VI (POTENTIAL).
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 826 850 VII (POTENTIAL).
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 915 AA; 102231 MW; F28AFC6454A6C2 CRC64;
 Query Match 5.2%; Score 348.5; DB 1; Length 915;
 Best Local Similarity 20.4%; Pred. No. 2e-16;
 Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;
 QY 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSELGAATWAVEHINR-KRLPGYTL- 196
 Db 44 RIEGDVTLGGLPVH-AKPGSGVPCGDIKRENGIHRLEAMLYALDQINDPLNPVTLG 102
 QY 197 -----ELVTNDTCQDPGVGVDRFFHAIYTOPSTRMVMILG 231
 Db 103 ARILDCSDRYALEQSLTFVQALLQKDTSDVRCNGE-----PPVFVKPE-KVGVIG 155
 QY 232 SACSEVTESLAKVVPYWNIVQVSFGSTSPALSDRRREFFYFRTVAPDSSHNPARIATIRK 291
 Db 156 ASGSSVSIWVANILRLFOIPQISYASTAPELSDRRYDFSRVVPDPSFQAQAMDIVKA 215
 QY 292 FGWGTVTTFSSQNEEVHSLAVNNLVTLEAANTSCAATITFAATDFKEQLL-----LL 343
 Db 216 LGWNYVTLASGSGYGERGVESFTQISKAGGLCIAQSVRIQERKDRITDFRIKQLL 275
 QY 344 RETDRIIIGSFQELAPQILCEAYLRMFGADYAWILHESMCAPWPDQRTACSNHEIQ 403
 Db 276 DTPNSRAVVIFANDEIDIKOILAAAKRADQVG-HFLWVGSDSWGSKINP-----LHOHE 327
 QY 404 LAVENLIVVSTHNSIVGNVSYGLNNHMFNSQLARKSQAFHQDGFSGYGPRIISAAT 463
 Db 328 DIAEGATIQPKRAV-----EGFDAFTSRTLENNRNRVFAEWEENFNCKLTISGS 381
 QY 464 QSDRRRRRRRGVVGSGHLPPEAI---SQYAPQ-----TYDAVMAIALALRAAEHWR 515
 Db 382 KKEDTDRKCTG-----QERIGKDSNYEQEGKVQFVIDAVYAMAHAL-----HMNK 427
 QY 516 N-----EQSKLDGFDYTRSDMAWEFLQOMKMLHFLGVSG-PSVFS-CPDRVGTTA 564
 Db 428 DLCAADYRGVCPCEMOAGG-----KLLKYIRHVNFGNSAGTPVFNKNGDAPGRYD 478

Db 698 LRSLOVGVVIAWLGAPP-----HSV-----IDYEQRTVDPQARGVLCNDSLSLIGCLG 750

Qy 807 YGGLLVGVVWAEWTRHVKIPALNDSQYIGCVSYSV-VITSALVVVLANLI--SERVTL 863

Db 751 YSLLLMVTCTVYAKARGVP-EFNEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYI 809

Qy 864 AFTITATILTSTATLCLLFIPLKLDI 891

Db 810 QTTTLVSLSLASVSLGMLIVPKTVI 837

RESULT 8

MGR2_HUMAN STANDARD; PRT; 872 AA.

AC Q14416;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 20-AUG-2001 (Rel. 40, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.

GN GRM2 OR GPRC1B OR MGLUR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95346007; PubMed=7620613;

RA Flor P.J., Lindauer K., Puttner I., Ruegg D., Lukic S., Knopfel T.,

RA Kuhn R.;

RT "Molecular cloning, functional expression and pharmacological

RT characterization of the human metabotropic glutamate receptor type

RT 2.;"

RL Eur. J. Neurosci. 7:622-629(1995).

CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS

CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC MAY MEDIATES SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN

CC SYNAPTOGENESIS OR SYNAPTIC STABILIZATION.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE

CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.

CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

CC STRONGEST. TO MGLUR3.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L35318; AAA76855.1; .

DR GCRDb; GCR.1846; .

DR MIM; 604099; .

DR InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCRMR.

DR PRINTS; PR00593; MTABOTROPICR.

DR PRINTS; PR01052; MTABOTROPICR.

DR PROSITE; PS00979; G-PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00980; G-PROTEIN_RECEP_F3_2; 1.

DR PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS02059; G-PROTEIN_RECEP_F3_4; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Multigene family.

FT SIGNAL 1

FT CHAIN 18

FT DOMAIN 19 872

FT DOMAIN 19 567

FT TRANSMEM 568 590

FT TRANSMEM 591 604

FT TRANSMEM 605 625

FT POTENTIAL.

FT METABOTROPIC GLUTAMATE RECEPTOR 2.

FT EXTRACELLULAR (POTENTIAL).

FT I (POTENTIAL).

FT CYTOPLASMIC (POTENTIAL).

FT II (POTENTIAL).

FT DOMAIN 626 636

FT TRANSMEM 637 655

FT DOMAIN 656 679

FT TRANSMEM 680 705

FT DOMAIN 701 725

FT TRANSMEM 726 747

FT DOMAIN 748 760

FT TRANSMEM 761 783

FT DOMAIN 784 793

FT TRANSMEM 794 819

FT DOMAIN 820 872

FT CARBOHYD 203 203

FT CARBOHYD 286 286

FT CARBOHYD 338 338

FT CARBOHYD 402 402

FT CARBOHYD 547 547

SEQ SEQUENCE 872 AA; 95507 MW; 058608C35C701E9D CRC64;

Query Match 5.2%; Score 349.5; DB 1; Length 872;

Best Local Similarity 21.8%; Pred. No. 1.6e-16;

Matches 188; Conservative 114; Mismatches 363; Indels 199; Gaps 31;

Qy 151 GKVLLGLFELSTSRPRPD-----GLSELGAATMAVEHINR-KRLPG----- 193

Db 30 GDLVGLGLFPVHQKGPACDCGVNEHRIQRLAMLFALDRINRDPHLLPGVRLGAHIL 89

Qy 194 -----YTLELVNTDTCDCPGVDPRPF-----AIYQPTRMVWLGSACSEVTE 239

Db 90 DSCSKDTHALQALDFVRASLRGADGSRHICPDGSIYATHGDAPTAITGVIGSISDVSI 149

Qy 240 SLAKVVPYNNIVQVSGSTSPALSDRRPEPFYFRTVAPDSSHNPARIAFIRKFGWTVT 299

Db 150 QVANLLRLFOIQAISYASTSAKLSDKYDFARTVPPDFEQAKAMAEILREFNNTYVST 209

Qy 300 FSONEEVSLAVNNLVTELEAANISCAATI-----TFAATDFEQL-LLRETDFRIIG 353

Db 210 EASEGDYGETGIEAFEELEAARANI-CVATSEKVGRAAFEGVVVRLALQKPSARVAVL 268

Qy 354 SFSQELAPQILCEAYRLRMFGADYAWILHESMGA----- 387

Db 269 FTRSEDARELLAASORL---NASFTWASDVGWGALESVAGSEGAEGAITIELASYPIS 325

Qy 388 -----PW-----WPDQRTACSNHQLQAVENLIV----- 412

Db 326 DFASYFQSLDPWNNRNPFREFW-EQRPFCFSFRQDCAAHSLRAVPPPEQSKIMFVVA 384

Qy 413 -----STHNSIVGNVSYSLNNHMFNSQLRKQSAQFHGQDGFSGYGPRIASIA 463

Db 385 VYMAHALHNHRLALCPNTRLCDDAMRPVNGRRLYK---DFVLNVKFDAPFRP---ADT 437

Qy 464 QDSRRRRRRGVGTSGGHLRPEALISQAPOTYDAVWATALALRAAEHRRNEEQSKLD 523

Db 438 HNEVRFDR-----FGDGIGRYNIFT-----LRAGSGRYRQKGVYNAE 476

Qy 524 GFDYTRSDMAWEFLQQMGKHLFVGSGVPSFSG-----PDRVGTGTAFOIGRLLEPVA 577

Db 477 GLTLDTSLPWASPS-----AGPLAASRCSEPCLONEVKSQVQCEVCWCWCIPQ 526

Qy 578 LYYPATDALDPRPCRPRVKWH-----SGQVPIAKRVFKLRVA-TIAPLAFYTIATLSSVG 632

Db 527 PYEYRLD--EFTCADCGLGYWPNASLTGCFELPQEIYRWGDWAVGPV---TIACLG--- 578

Qy 633 IALAITF-LANLHFRKLKAIKLSFKPKLSNITAVGCIFFYATVILLGLDHSILPSAESDF 691

Db 579 -ALATFLVLGVFVVRHNATPVVKAAGRELCYLLGGVFLCYCMTFIIFAKSP----- 629

Qy 692 ATVCTARVYLLSAGFSLAGFSGMAFYRVHRIF--TRTGSVFKDKMLQDIQILLVGLGL 749

Db 630 -AVCTLRRLGLGTAFSCVYSALLYTKNIARIFGGARGAQ-RPRFISPASOVAICLALI 687

Qy 750 LVDALLVTLWVYVTPDPMERHLNHLNLTLEISATRSVV-YOPQVEVCRSQHTQTWLSVLYAYK 808

Db 707 LQVVGMTANLGRPP-----HSV---IDYEQRTVDPEARGVLKCDMSDLSLIGCLGYSL 759
 QY 810 LLLVGVYMAWETRVKIPALNDQYIGSVYSV-VITSAIVVVLANLI--SERVTLAFI 866
 Db 760 LLMTVCTVYAIKARGVP-ETNEAKPIGFTMTWTCIIWLAFVPIFFGTGAQSAEKIYIQT 818
 QY 867 TITAIITSTATLCLFIPKLDI 891
 Db 819 TLTVSLSLASVSLGMLYVPKTYVI 843

RESULT 7
 MGR6_RAT - STANDARD; PRT; 871 AA.
 AC P35349;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
 GN GRM6 OR GPRC1F OR MGLUR6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Retina;
 RX MEDLINE=93280152; PubMed=8389366;
 RA Nakajima Y., Iwakabe H., Akazawa C., Nawa H., Shigemoto R.,
 RA Nakanishi S.;
 RT "Molecular characterization of a novel retinal metabotropic glutamate
 RT receptor mGluR6 with a high agonist selectivity for L-2-amino-4-
 RT phosphonobutyrate.";
 RL J. Biol. Chem. 268:11868-11873(1993).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR
 CC LAYER OF THE RETINA.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13963; BAA03066.1; -
 CC PIR: A6742; A46742.
 CC GCRdb: GCR_0623; -
 CC InterPro: IPR001828; ANF_receptor.
 CC InterPro: IPR000337; GPCR_Mgr.
 CC Pfam: PF00003; 7tm.3; 1.
 CC Pfam: PF01094; ANF_receptor; 1.
 CC PRINTS: PR00248; GPCR_MGR.
 CC PRINTS: PR00593; MTABOTROPICR.
 CC PRINTS: PR01056; MTABOTROPICR.
 CC PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
 CC PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
 CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
 CC PROSITE: PS02059; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Vision.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 871 METABOTROPIC GLUTAMATE RECEPTOR 6.
 FT DOMAIN 19 579 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 580 602 I (POTENTIAL).
 FT DOMAIN 603 616 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 617 637 II (POTENTIAL).
 FT DOMAIN 638 648 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 649 667 III (POTENTIAL).
 FT DOMAIN 668 691 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 692 712 IV (POTENTIAL).
 FT DOMAIN 713 742 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 743 764 V (POTENTIAL).
 FT DOMAIN 765 777 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 778 800 VI (POTENTIAL).
 FT DOMAIN 801 813 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 814 839 VII (POTENTIAL).
 FT DOMAIN 840 871 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;

Query Match 5.5%; Score 367; DB 1; Length 871;
 Best Local Similarity 21.8%; Pred. No. 9.1e-18;
 Matches 189; Conservative 130; Mismatches 361; Indels 188; Gaps 32;

QY 151 GKVLGLGFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLLPG----- 193
 Db 31 GGLTGLGLFPVH-ARGAAGRACGALKKEQGVHRLEAMLYALDRVNNADPELLPGVRLGARL 89
 QY 194 -----YTLELVNTDQ-----CDPGGVDRFFHAYITOPSTRMVMLL 230
 Db 90 LDTCSRDTYALQALSFVQALIRGDCDEASVRCPGV-----PPURSPAPPVRVAVV 143
 QY 231 GSACSEVTESLAKVVPVNNIVQVSGTSPALSDRRFFPYFYRTVADSSHPNARIAFI 290
 Db 144 GASASSVSIWVNVRLFAIPQISYASTAPELSDSTRYDFESRVVPPDSYQAQAMVDIVR 203
 QY 291 KFGWGTVTTSQNEVHSLAVNNLY-TELEAANISCAATITFAAT-----DFKEQLLLIRE 345
 Db 204 ALGWNVYSTLASEGNYGESGVEAFVQISREAGGVCAIOSIKIPREPKEPFKVRIRLME 263
 QY 346 TDRIRIIGSFQOELAPOLCEAYRLRMFGADYAWTLHSGMGPWWPDQRTACSNHELQLA 405
 Db 264 TPNARGIIIFANEDDIRRVLEATQANLTGHFLVGSWSGKISP-----ILNLE 314
 QY 406 VENLIVVSTHNSIVGNVSYGLNNHMFNSQLRKQSAQFHQDGFSGYGPRIATAAQS 465
 Db 315 EEAVGAI---TILPKRASIDGFDQYFMTSRLENRRNRIWFAEFWENFNCKLTSSGGS 370
 QY 466 DSRRRRRGVVGTSGHGLFPAISQ---YAPQ-----TYDAVWAIALRAAE----- 511
 Db 371 DDSTRKCTG-----EERIGDSAYEQEGKVQFVIDAVYATAHALHSMHQALCPGH 420
 QY 512 -----HWRR-----NEEQSKLDGFDY----- 527
 Db 421 TGLCPAMEPTDGRITLLHYIRAVRNGSAGTVPVFNENGDAPGRYDIFQYQATNGSASSG 480
 QY 528 -----TRSDMAWEFLQOMKGLHPLGVSGPVSVFSGDPDRVGTFATYQIQRGLLEPVA 577
 Db 481 YQAVGQNAEALRLDM--EVLNWSGDPHEV---PPSQCSLP--CGPGERKKWKGV--PCC 531
 QY 578 LYPATDAL-----DFRCPRC-----RPVKHSGGVPIAKRVFKLKVATIAPIAFYTIATL 628
 Db 532 WHCEACDGYRFQVDEFTCEACPGDMRPTPNHTGCRPTP---VRLTWSSPWAALPL-LL 586
 QY 629 SSVGIALAIYFLAFNLHFRKKAIKLSPKLSNITAVCCIFVATVILLGDHSLTPSAE 688
 Db 587 AVLIGMATTTIMATFMRHNDTPVIVRASGRELSVLLTGIFLIYAITFLM-----VA 637
 QY 689 DSFATVCTARVYLLSAGFSIAFGSMFAKTYRVHRITFR-TGSVFKDKMLQDILILLVGG 747
 Db 638 EPCAICAARLLGLGLTLLSYLSALLTKNRIYRIFEOGKRKSVTPPPFISPTSQLVITFG 697
 QY 748 LLLVDALLVTLVWVTDPMERHLNLTLEISATDRSVVYQPOVE-VCRSQHOTVTLVSLVA 806

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Qy 802 -----SVLYAYKGLLVGVYMAWETRHVKIPALN 831
Db 771 ELWSFAVSDVQRATVGGSPICVWPAPESIFYGYKGLLLGIFLAYEYKSVSTEKIN 830
Qy 832 DSOYIGSVYSVVITSIAVVVLANLISERVTLAFITITLITLTTATLCLLIPKLDHI 891
Db 831 DHRAGMAIYNVAVLCITAPVTMILSSQDAAFAFASLAIVFSSYITLVVLFVPMKRL 890
Qy 892 WARNDIIDPVIHSMGLKMECNTRFVVDDRELOQYRVEVQNRVYKEIQALDAIRKLER 951
Db 891 ITRGEQWSETQDTMKTGSSSTN-----NNEEKSRLEKENRELEKIIAEKEERVSELRH 944
Qy 952 LLES 955
Db 945 QLOS 948

RESULT 6
MGR6_HUMAN
ID MGR6_HUMAN STANDARD; PRT; 877 AA.
AC O15303;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR GPRC1F OR MGLUR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358610; PubMed=9215706;
RA Hashimoto T., Inazawa J., Okamoto N., Tagawa Y., Bessho Y., Honda Y.,
RA Nakanishi S.;
RT "The whole nucleotide sequence and chromosomal localization of the
RT gene for human metabotropic glutamate receptor subtype 6."
RL Eur. J. Neurosci. 9:1226-1235(1997).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U82083; AAB82068.1; -.
CC GCRdb; GCR_2607; -.
CC MIM: 604096; -.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01056; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_5; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Vision.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 877 METABOTROPIC GLUTAMATE RECEPTOR 6.
FT DOMAIN 25 585 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 586 608 I (POTENTIAL).

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FT DOMAIN 609 622 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 623 643 II (POTENTIAL).
FT DOMAIN 644 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 673 III (POTENTIAL).
FT DOMAIN 674 697 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 698 718 IV (POTENTIAL).
FT DOMAIN 719 748 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 749 770 V (POTENTIAL).
FT DOMAIN 771 783 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 784 806 VI (POTENTIAL).
FT DOMAIN 807 819 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 820 845 VII (POTENTIAL).
FT DOMAIN 846 877 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 296 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 451 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 479 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 567 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 877 AA; 95436 MW; AECDF91E8DA5994F CRC64;

Query Match 5.5%; Score 372; DB 1; Length 877;
Best Local Similarity 21.6%; Pred. No. 4.1e-18;
Matches 187; Conservative 132; Mismatches 364; Indels 182; Gaps 30;

Qy 151 GKIVLLGLFEL-----STSRGP--RPDGLSELGAATMAVEHINR-KRLLPG----- 193
Db 37 GGLTGLGLFPVHARGAAGRACGLKKEQGVHRLAMLYALDRVNADPELLPGVRLGARLL 96
Qy 194 -----YFLELVNTDTC-----DPGCVDRFFHAIYTPSTRMVLGSCACSEV 237
Db 97 DTCSDRTYALEQALSFVQALIRGRGDGVGRCGVPLRPAPPERRVAVVVGASASSV 156
Qy 238 TESLAQVVPYWNIVQSGTSPALSDREFFYFRTVAPDSSHNPARIATIRKFGWTV 237
Db 157 SIWVANVLRLEAIPOISYASTAPELSDSTRYDFFSRVPPDSYQAQAMVDIVRALGMNV 216
Qy 298 TTFSONEEVHSLAVNNLV--TELEAANISCAAITFAAT-----DFKQLLLRLTDRIRII 352
Db 217 TSLASEGNYGESGVFAFVQISREAGGVCIQSIKIPREPKPGEFSKIVIRLMETPNARGI 276
Qy 353 GFSFSELAPOILCEAVRLRMFGADYAWILHESMGAPWPDQRTACSNHEILOLAIVENLV 412
Db 277 IIFANEDDIRRVLEAARQANLTGHFLWVGSDSWGAKTSP-----ILSLEDVAVG 325
Qy 413 STHNSIVGNVNSYGLNNHMFNSQLKQSAQHFQDGGFGSGYGPRIASIAATQSDSRRRR 472
Db 326 AI--TILPKRASIDGFDQYFMRSLNNRNRIWFAEFEEFNCKLTSSGTQSDSTRKC 383
Qy 473 RGVGTSGHLPPEAISQVAPOTY-----DAVWAIALAAEE-----HWRNRE 517
Db 384 TG-----EERIGR--DSTYEQEGKVQFVIDAVYAIHAHSMHQALCPGHTGLCP 431
Qy 518 EQSKLDGDFDTRSDMAWEFLQOMKLIHFGVSG-PVSFS-GPDRVGTTFATFYIQ----- 569
Db 432 AMEPTDG-----RMLQYIRAVRFGSAGTPVMFNENGADPGRYDIFQATNGSA 482
Qy 570 -----RGLLEPVALLY 580
Db 483 SSGGYQAVGQMAETLRLDVEALQWSDPHEVPSSLCSLPCGPGERKKMKVGV--PCWHC 540
Qy 581 PATDAL-----DFRCPRC-----RPVKWHSGQVPIAKRVEKLRVATIAPIATYIATLSSV 631
Db 541 EACDGYREFQVDEFTCEACPGDMRPTPNHTGCRPTP-----VRLSWSSPWAAPPL-LLAVL 595
Qy 632 GIALAITFLAFNLHFKLKAIKLSSPKLSNITAVGCFIVYATVILLGLDHSHTLPSAEDSF 691
Db 596 GIVATTVYATVFRVYNNTPIVRASGRELSYLLTGTLFIYAITFLM-----VAEPG 646
Qy 692 ATVCYARVYLLSAGFSLAFSGSMFAKTYRVHRIFTR-TGSVFKDKMLQDILQILLVGLLL 750
Db 647 AAVCAARRLFGLGTLSYSALLTKTNRIYRIFEQGRSVTPPPFISPTISQLVITFSLIS 706
Qy 751 VDALLVTLMVVDPMERHLNLTLEISATDRSVVYQPOVE-VCRSHTQTWLSVLYAYKG 809

```

CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC LINKER HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC -!- CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF.3.
 CC -----
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 CC -----
 CC EMBL; Y10369; CAA71398.1; -.
 CC EMBL; Y10370; CAA71399.1; -.
 CC EMBL; AB016160; BAA34708.1; -.
 CC EMBL; AB016161; BAA34709.1; -.
 CC EMBL; AF110797; AAD19656.1; -.
 CC EMBL; AF110796; AAD19656.1; JOINED.
 CC EMBL; AF110797; AAD19657.1; -.
 CC EMBL; AF110796; AAD19657.1; JOINED.
 CC EMBL; AF110797; AAD19658.1; -.
 CC EMBL; AF110796; AAD19658.1; JOINED.
 CC EMBL; AF110797; AAD19659.1; -.
 CC EMBL; AF110796; AAD19659.1; JOINED.
 CC HSP; P10998; 1VVC.
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00003; 7tm3_1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC Pfam; PF01084; sushi; 2.
 CC PRINTS; PR01176; GABARECEPTR.
 CC PRINTS; PR01177; GABARECEPTR.
 CC SMART; SM00032; CCP; 2.
 CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 CC SIGNAL 1 16
 CC CHAIN 17 991
 CC
 CC DOMAIN 17 590
 CC TRANSMEM 591 611
 CC DOMAIN 612 630
 CC TRANSMEM 631 651
 CC DOMAIN 652 666
 CC TRANSMEM 667 687
 CC DOMAIN 688 709
 CC TRANSMEM 710 730
 CC DOMAIN 731 797
 CC TRANSMEM 798 818
 CC DOMAIN 819 834
 CC TRANSMEM 835 855
 CC DOMAIN 856 863
 CC TRANSMEM 864 884
 CC REPEAT 29 95
 CC REPEAT 99 156
 CC DOMAIN 885 991
 CC DOMAIN 901 955
 CC CARBOHYD 23 23
 CC CARBOHYD 83 83
 CC CARBOHYD 408 408
 CC CARBOHYD 439 439

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 163 MLLLVPLFLRLPLGAGQPTNATSEGCQIHPWEGGIR
 FT YRLTRQVKAINFLPDVDEYEVVCRGEVGVKVKCLA
 FT NGSTDMTPSRVCYRICKSVLTLENKVFLLTGGDPAIDG
 FT ARVECPDPPHLVSSRSVCQSQGWSTP-KPHCQVNRTPH
 FT -> MGPGCPPTVGMPLPLLLVMAAGVAPVWASHSPHLP
 FT HPRVPHPS (IN ISOFORM 1B, ISOFORM 1C AND
 FT ISOFORM 1D).
 FT MISSING (IN ISOFORM 1A, ISOFORM 1B AND
 FT ISOFORM 1D).
 FT KEERVELHQQRQQLRRRHPTTPDPDGGGLPRGSEPE
 FT PDLRSCDGRVHLLYK -> VCGDKQPGPVSEGLPVVGP
 FT SIEV (IN ISOFORM 1D).
 FT S->A: NO CHANGE IN THE AFFINITY FOR GABA.
 FT MUTAGEN 247 247 S->A: NO CHANGE IN THE AFFINITY FOR GABA.
 FT MUTAGEN 268 268 S->A: NO CHANGE IN THE AFFINITY FOR GABA.
 FT MUTAGEN 269 269 S->A: DECREASE IN THE AFFINITY FOR GABA.
 FT SEQUENCE 991 AA; 111533 MW; 012CD293D4B44A2 CRC64;

Query Match 14.5%; Score 971; DB 1; Length 991;

Best Local Similarity 28.7%; Pred. No. 3 6e-60;

Matches 259; Conservative 157; Mismatches 364; Indels 124; Gaps 18;

QY 96 RROQLNSHNLPGSTNASHAHLLNLPQRORYLKVNQVFESERRMSPAEMQRNHGKIVL 155
 DB 125 RVEFRCDPDPFHLVGGSSRSVCQGWSTP-KPHCQVNRTPHSERR-----AVYI 171
 QY 156 LGLFELSTSRGPRDGLSELGAATMAVEHINRKR-LLPGTYLELVNTDQCDPQGVGVDRF 214
 DB 172 GALEPMS---GGWPGGQACQPAVEMALADVNSRRDILPDYELKLIHDSKCDPGQATKYL 228
 QY 215 FHAIYTOPSTRMVMVLGSAQSEVTESLAKVVPYVNIQVSEGSTSPALSDREFFYFRT 274
 DB 229 YELLYNDP---IKIILMPGCSVSTLVAEAAARMWNLVLSYSSSPALSNRQFFTFRT 285
 QY 275 VAPDSHNPARIATIRKFGWGTVTTFQNEEVHSLAVNLVTELEAANISCAATITFAAT 334
 DB 286 HPSATLHNPTRVKLFKEGWKKIATIQTTVEFTSTLDDLEERVKEAGIE---ITFRQS 341
 QY 335 DFEQQL---LLRETDTRIIGSFSQELAPQILCBAYRLRMFGADYAWILHESMGAPWMP 391
 DB 342 FFSDPAVPVKNLKRQDARIIVGLFVETEARKVFCVEYKRLFGKKYVWFLGIWYADNWFK 401
 QY 392 --DQRTACSNHELOLAVENLIVVSTHNSIVGNVSYSGLNHHMFSQLRKQSAQFHQDG 449
 DB 402 TYDPSINCTVEEMTEAVEGHITTEIVMLNPANTRISNMTSQEFVEKLTG-----451
 QY 450 FGSGYGPRIATAATQSDSRRRRRGVGTSGHLPPEAISOVAPQTYDAVMAIALRAA 509
 DB 452 -----RLKRHPETGG-----FQEAPLAYDAIWAALALAKNT 483
 QY 510 EHWRRNEEQSKLDGFDYTRSDMAWEFLQOMKGLHLFVGSGPVSF-SGPDRTVGTTFATYQI 568
 DB 484 SGGGGRS--GVRLEDFTNNQITTDQIYRAMSSSFEVSGVGHVFDASGRMAWTLIEQL 541
 QY 569 QRGILLEVALYYPATDALDFRCPRCPVKWHSGQVPIAKRVKLRVATIAPIAFYTIATL 628
 DB 542 QGSYKKIGYYDSTKDDLSW---SKTDKWIWGSPADQTLVIKTRFLSQKLFISVSYL 597
 QY 629 SSVGIALAITFLAFNLHFRKLKATIKLSPKLSNITAVGCFIVYATVILLGDHSTLPSAE 688
 DB 598 SSLGIVLAVCLSNFYNSHVRYIQNSQPNLNLNTAVGCSLALAAVFLGLDGYHI--GR 655
 QY 689 DSFATVCTARVYLLSAGFSLAFGSMFAKTYRVHRITRTGVSFKD-----KMLQDIQILI 742
 DB 656 SQPFVVCQARLWLLGLGSLGYSMTFKIWWVHTVFTK-----KEEKREWRKTLPEWKLY 710
 QY 743 LLVGGLLLVALLTVLWVVTDPMERHLNLTLEISATDRSVVYQPVQVCRSQHTQTLW- 801
 DB 711 ATVGLLVGMDVLTAIQWIDPDLPHRTIETFAKEPKEDIDVSLPQLEHSCSKKMTWLIG 770

QY 454 YGPRISIAATQSDRRRRRRRGVGTSGHLPPEAISQAPQTYDAVNAIALARAEEHW 513
 DB 452 -----RLKRHEETGG-----FOEAPLAYDAIWAIALAKNTSGG 487
 QY 514 RRNEEQSKLGFEDYTRSDMAWEFLQOQKHLFGLVSGPVSP-SGPDVRGTTAFYQIORGL 572
 DB 488 GRS--GVRLEDFNYNQTTDQIYRANSSSEFGVSGHVFDASGRMAWTLIELOQGG 545
 QY 573 LEPAVALYPATDALDFRCPRCPVKWHSQGVPIAKRVFKLRVATIAFLAFYTIATLSVG 632
 DB 546 YKIGIYDSTKDDLSM---SKTDKWIGSGPPADQTLVKTFRFLSQKLFISVSLSLG 601
 QY 633 IALATFLAPNLHFRKLKALKSPKLSNITAVGCIFFVATPVILLGDHSLPLSAEDSFA 692
 DB 602 IVLAVCLSEFNINSHVRYIQNSQPNENLTAVGCSLALAAVFLPLGLDGYHI--GRSQFP 659
 QY 693 TVCTARVYLLSAGFSLAFSGMEAKTYVHRLFTRTGVSFKD-----KMLQDIQLILLVG 746
 DB 660 FVCOARLWLLGLGFLSGYSGMFTKIMWVHTFK-----KEEKKEWRTLEPWKLATVG 714
 QY 747 GLLVDALLVTLVAVDPMERHLHLNLTLEISATDRSVVYQPVQVEVCRSOHTQWLSVLYA 806
 DB 715 LVGMDLTLTAIQVDPHLRTTETFAKEPKEDIDVSLPQLEHCSKKNWTLGIFYG 774
 QY 807 YGGLLVGVYMAWEHRVHKIPALNDSQYIGSVYSVVTSAIYVVVLANLISERVTLAFI 866
 DB 775 YKGLLLGLIFLAYETKSVSTEKINDHRAVGMATYNAVLCILITAPVTMILSSQDDAFA 834
 QY 867 TITALLITSTATLCLLFIPLKLDIWARNDIIDPVHSMGLKMECNTRFVVDDBRELQY 926
 DB 835 FASLAIYFSSYITLVFLVFPKRLITRGEMQSEADQTMKTGTSNT-----NNEEKSR 888
 QY 927 RVQNRVYKKEIQALDAERKLERLES 955
 DB 889 LLEKENRELEKIATAEERYSERLHQLOS 917
 RESULT 5
 GBRL_RAT STANDARD: PRT: 991 AA.
 ID GBRL_RAT STANDARD: PRT: 991 AA.
 AC Q92004; Q08620; Q08621; Q920F9; Q92308;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
 DE RECEPTOR 1) (GABA-B-RL) (GB1).
 GN GABRL.
 OS Rattus norvegicus (Rat).
 QC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN-RICO; TISSUE=brain cortex, and Cerebellum;
 RX MEDLINE=9722131; PubMed=9069281;
 RA Kaupmann K., Huggel K., Heid J., Flor P.J., Bischoff S., Mickel S.J.,
 RA McMaster K., Augst C., Bittiger H., Froestl W., Bettler B.;
 RT "Expression cloning of GABA(B) receptors uncovers similarity to
 RT metabotropic glutamate receptors.";
 RT Nature 386:239-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99092370; PubMed=9875211;
 RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
 RA Iano K., Taniyama K.;
 RT "Cloning and tissue distribution of novel splice variants of the rat
 RT GABAB receptor.";
 RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1E).
 RC STRAIN-Wistar; TISSUE-Hippocampus;

RX MEDLINE=99388283; PubMed=10457184;
 RA Pfaff T., Malitschek B., Kaupmann K., Prezeau L., Pin J.-P.,
 RA Bettler B., Karschke A.;
 RT "Alternative splicing generates a novel isoform of the rat
 RT metabotropic GABA(B)R1 receptor.";
 RL Eur. J. Neurosci. 11:2874-2882(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND 1A-R2 INTERACTION.
 RC TISSUE=Brain;
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chatauneuf A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RL J. Biol. Chem. 274:7607-7610(1999).
 RN [5]
 RP TISSUE DISTRIBUTION.
 RX MEDLINE=20121644; PubMed=10658574;
 RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
 RA Ng G.Y.K.;
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
 RT forms.";
 RL Bioorg. Med. Chem. 7:2697-2704(1999).
 RN [6]
 RP 1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";
 RL Science 283:74-77(1999).
 RN [7]
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
 RX MEDLINE=20159055; PubMed=10692480;
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
 RA Kaupmann K., Pin J.-P.;
 RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)
 RT binding at GABA(B) receptors: involvement of serine 269 of the
 RT GABA(B)R1 subunit.";
 RL Mol. Pharmacol. 57:419-426(2000).
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTI-NOCEPTION.
 CC -1- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-RL AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-RL AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-RL TO THE
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A, 1B, 1C, 1D AND 1E (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS. GRANULAR CELL
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS

FT	TRANSMEM	710	730	IV (POTENTIAL).	
FT	COMAIN	731	767	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	768	788	V (POTENTIAL).	
FT	DOMAIN	789	803	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	804	824	VI (POTENTIAL).	
FT	DOMAIN	825	832	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	833	853	VII (POTENTIAL).	
FT	DOMAIN	854	960	CYTOPLASMIC (POTENTIAL).	
FT	REPEAT	29	95	SUSHI 1.	
FT	REPEAT	99	156	SUSHI 2.	
FT	DOMAIN	868	924	COILED COIL (POTENTIAL).	
FT	CARBOHYO	23	23	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	83	83	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	408	408	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	439	439	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	481	481	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	501	501	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	CARBOHYO	513	513	N-LINKED (GLCNAC. .) (POTENTIAL).	
FT	VARSPLIC	1	163	MLLLLLVPLFLRPLGAGGAQTPNVTSEGCIIHPHWEGLGIR YGLGRVOOKAFLNPLVOYEIVCGREREVVGPKVRKCLAL NGSNWTDMPSPRCVRCISKXYLTLENGKVFLTGGDLPAOC ARVOECDDPDLHVLGSSRSICSQGQWSTPKPHCQVNRTPH -> MGPGGDDPVGWPLPLLVLLVMAAGVAPVWASHPLPR HPRVPPHPS (IN ISOFORM 1B, ISOFORM 1C AND ISOFORM 1O).	
FT	VARSPLIC	771	960	IFVYGLGILLGLIAYETKSVSTEKINDHRAVGMATYIN AYGLCLTAPVTMLSSQOAAFAFLAIVFSSVITLVLE VPMRLRLTRGEMQEAQDTWKTSSTNNNEEKSRLLKE NNEKLKILAEKERVSEHLQHQSRIRRHPTTPDPDS GGIPGPPSPORLSCOGSRVHLLYK -> ELW5FCCE (IN ISOFORM 1C).	
FT	VARSPLIC	904	960	KEEYRVSSELHQLOSRQOIRSRHPTTPPOPSGGLPRGPSE PORLSCDGSRVHLLYK -> VCGQNGPLSGRLSVAPQV QOVLVYIGSGKACGAGERKGG (IN ISOFORM 1O).	
FT	CONFLICT	7	8	VP -> LL (IN REF. 1).	
FT	CONFLICT	46	46	T -> I (IN REF. 1).	
FT	CONFLICT	618	618	V -> A (IN REF. 1).	
FT	CONFLICT	642	642	A -> V (IN REF. 1).	
FT	CONFLICT	721	721	I -> V (IN REF. 1).	
FT	CONFLICT	812	812	A -> P (IN REF. 3 AND 4).	
FT	CONFLICT	869	869	A -> T (IN REF. 1).	
FT	CONFLICT	921	921	I -> L (IN REF. 1).	
FT	SEQUENCE	960 AA;	108216 MW;	E4B5A94.01E23E8B4 CRC64;	
Query Match					14.8%; Score 990.5; DB 1; Length 960;
Best Local Similarity					29.6%; Pred. No. 1.4e-61;
Matches 257; Conservative 156; Mismatches 363; Indels 93; Gaps					
Qy	100 RLNSHSLPGSTWASHAHLNLLPPRQRYLYKNQVSESRMSPAEQMORHCKVILLGLF	159			
Db	129 RCDPQHLVGGSSRSICSGQWSTP--KPHCQVNRTPHSERR-----AVYIGALF	175			
Qy	160 ELSTSRGPRPGISLGAATPAVEHINRRK-LLPGYTLELVNTDQCQDVGVDVFFHAI	218			
Db	176 PMS--GGWPGGQACQAVEMALEOVNSRROILPDYELKLIHDSKCPGQATKYIELL	232			
Qy	219 YTPQSTRMWMLLGSACEVTESLAKVVPYVNIQVSGFSTSPALSDRRREFFYFTVAPD	278			
Db	233 YNOP---IKIILPGCCSSVTLVAEAAARNWLIVLISYSGSSPALSNRQRFPTFFRTHPS	289			
Qy	279 SSHNPARIATIRKFGCTVTTFSQNEEVHSLAVNNLVTELEAANTSCAATITFAATOPKE	338			
Db	290 TLHNPTVKVLFERKWMKKIATIQQTTEVTSTLODLEERVKKAGIE---ITFRQSFSS	345			
Qy	339 QLL---LLRETORTIRIGGSQELAPQILCEAYRLRMGAOAVAILHESMGAPMWP--DQ	393			
Db	346 PAVPVKMLKQDARIIVGLGYETEARKVCEVYKELFGKKYVWFLIGHYAOHWFKTYDP	405			
Qy	394 RTACSNHELQAVENLIVVSTHNSIVGNVYSGLNHNHMFNSQLRKQSAQFHGQDGFSG	453			
Db	406 SINTVEEMTEAVEGHLTITTEIVMLNPANTFRSINMTSOFVEFKIYK-----451				

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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@sib-sib.ch).

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DR EMBL; AJ225028; CAA12359.1; -
DR EMBL; AJ225029; CAA12360.1; -
DR EMBL; AJ012185; CAA09939.1; -
DR EMBL; AJ012186; CAA09940.1; -
DR EMBL; AF099148; AAC98508.1; -
DR EMBL; Y11044; -; NOT_ANNOTATED_CDS.
DR EMBL; AJ012187; CAA09941.1; -
DR EMBL; AJ010170; CAA09031.1; -
DR EMBL; AJ010171; CAA09031.1; JOINED.
DR EMBL; AJ010172; CAA09031.1; JOINED.
DR EMBL; AJ010173; CAA09031.1; JOINED.
DR EMBL; AJ010174; CAA09031.1; JOINED.
DR EMBL; AJ010175; CAA09031.1; JOINED.
DR EMBL; AJ010176; CAA09031.1; JOINED.
DR EMBL; AJ010177; CAA09031.1; JOINED.
DR EMBL; AJ010178; CAA09031.1; JOINED.
DR EMBL; AJ010179; CAA09031.1; JOINED.
DR EMBL; AJ010180; CAA09031.1; JOINED.
DR EMBL; AJ010181; CAA09031.1; JOINED.
DR EMBL; AJ010182; CAA09031.1; JOINED.
DR EMBL; AJ010183; CAA09031.1; JOINED.
DR EMBL; AJ010184; CAA09031.1; JOINED.
DR EMBL; AJ010185; CAA09031.1; JOINED.
DR EMBL; AJ010186; CAA09031.1; JOINED.
DR EMBL; AJ010187; CAA09031.1; JOINED.
DR EMBL; AJ010188; CAA09031.1; JOINED.

Query Match      14.8%; Score 991.5; DB 1; Length 961;
Best Local Similarity 29.6%; Pred. No. 1.2e-61;
Matches 257; Conservative 157; Mismatches 362; Indels 93; Gaps 17;

QY 100 RUNSHNLPSTNASHAHLLNLPORLYLKVNQVFESERMSPAEMORNHGKLVLLGLF 159
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DB 130 RCDPDLHLVSGSSICSGQWSTP--KPHCVNRTPHSERR-----AVYIGALF 176

QY 160 ELSTSGPRPDGLSELGAATMAVEHINRKR-LLPGYILELVNTQCDPGVGVDPRFTHAI 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 177 PMS---GGMPGGACQAPVEMALDVSRRDILPDYELKLIHHDKCDPGQATKLYELL 233

QY 219 YTOPSTRMVMLLGSACSEVTESLAKVVPYVNIQVSGSTSPALSDRRRPFYRTVAPD 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 234 YNDP---IKIILMPGSSVSTLVAARMWNLIIVLSGSSPALSNRQRPFTFFRTHPSA 290

QY 279 SSHNPARIAFIRKFGWGTVTTFSSQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKE 338
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DB 291 TLHNPTRVKLFEXGWKKIATIQOTTEVFTSLDDELRVKEAGIE---ITFRQSFFSD 346

QY 339 QLL---LLRETDFRIIGTSQELAPOLCEAYRLRMFGADYAWILHESGAPWMP--DQ 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 347 PAVPVNKLKQADRIIVGLFYEATKRVFCEYKERLFGKYVWFLGICWYADNFKIYDP 406

QY 394 RTACSNHEQLQAVENILVSVTHNSIVGNVSYSLNHNMFNSQLRKOSQAFHGQDGTGSG 453
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DB 407 SINCTVDEMTFAVEGHITTEIVMLNPANTRSINMTSQQEFVEKLTK----- 452

QY 454 YGPRISIAATQSDRRRRRRRGVGTSGGHLFPFAISQYAPQTYDAVNAIALRAAEHWH 513
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 453 -----RLKRHPETGG-----FQEAFLAYDAIWAIALANKTSGGG 488

QY 514 RNEEQSKLDGFDYTRSDMAWEFLQMGKLUHFLGVSGPVSF-SGPDRVGTGTAFVQIQRL 572
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DB 489 GRS--GVRLEDNFYNNQITDQIYRAMSSSFEVSVGHVVDASGRMAWTLIEQLQGS 546

QY 573 LEPVALIYPATDALDFRCRCRPVWHSGQVPIAKRVFKLRVATIAPLAYTITLSSVG 632
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DB 547 YKGIKYDSTKDDLSW-----SKTDKWTGGSPPADQTLVIKTRFLSKQLFISVSLSLG 602

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QY 633 IALAITFLAFNLHFRKLKRAIKLSSPKLSNITAVGCIFFVYATVILLGLDHSITLPSAEDSTA 592
DB 603 IYLVAVVCLSFNFIYQNSQPNLNNLTAVGCSLAAAFPLGLDGYHI--GRNQPP 560
QY 693 TVCTARVYLLSAGSFLAFSGMFAKTVRVHRIETRTGVSFKD-----KMLQDIQILLLVG 746
DB 661 FVCQARLLWLLGLGFLSGYSGMFTKIWWVHTVTK-----KEKKWRKLTLPWKLYATVVG 715
QY 747 GLLVLDALLVTLWVYVTPMERHLNLTLEISATDRSVVYQPVQVCRSQHTQTLWSVLXA 806
DB 716 LLVAGMDVLTALAIQIWDPLHRTIETFAKEPKEDIDVSLPQLCHCSSRKMNTWLGIFVG 775
QY 807 YKGLLLVGVYMAWETRVHKIPALNDSQVIGSVYSVITSAIVVLANLISERTVLAFI 866
DB 776 YKGLLLGLIFLAYETKSVSTEKINHRAVGAIVNAVVLITIPVTVTILSSQDDAAPA 835
QY 867 TITALLTSTTATLCLLFIPLKLDIWARNDIIDPVHSMGLKMECNTRFVVDDRRLEQY 926
DB 836 FASLAIVFSSYITLVLPVKMRRLITRGEWQSEAOQTMKTGSTN-----NNEEKSR 889
QY 927 RVEQNVRYKQIQAIDAEIRKLERLES 955
DB 890 LLEKENRELEKIIAEKEERSVSELRHQLOS 918

RESULT 4
GBRL_MOUSE
ID GBRL_MOUSE STANDARD; PRT: 960 AA.
AC Q9WV18; Q9WV15; Q9WV16; Q9WV17; Q9WU48;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GB1).
GN GABBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier M., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RA "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RL receptor.";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1B).
RX Younger R.;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1B).
RA Lamp K., Humeny A., Nikolic Z., Becker C.-M.;
RT "Cloning of the murine GABABR1b receptor.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RA Humeny A., Lamp K., Nikolic Z., Becker C.-M.;
RT "Mouse GABA-B receptor cDNA sequence.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP R1A-R2 INTERACTION.
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of heteromer formation in GABAB receptor function.";
RL Science 283:74-77(1999).
CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.

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RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99087321; PubMed=9872316;
 RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
 RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
 RT "Heterodimerization is required for the formation of a functional
 RT GABA(B) receptor.";
 RL Nature 396:679-682(1998).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP TISSUE=Brain;
 RC Stropp U., Raming K.;
 RA "Human mRNA for GABA-B1a receptor.";
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP TISSUE=Fetal brain;
 RC MEDLINE=98440782; PubMed=9753614;
 RX Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,
 RA Zelante L., Gasparini P.;
 RT "GABA (gamma-amino-butyric acid) neurotransmission: identification and
 RT fine mapping of the human GABAB receptor gene.";
 RL Biochem. Biophys. Res. Commun. 250:240-245(1998).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP MEDLINE=99014802; PubMed=9798068;
 RX Gei V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,
 RA Gruen J.R.;
 RT "Human gamma-aminobutyric acid B receptor gene: complementary DNA
 RT cloning, expression, chromosomal location, and genomic organization.";
 RL Biol. Psychiatry 44:659-666(1998).
 [6]
 RN SEQUENCE FROM N.A. (ISOFORM 1C).
 RP TISSUE=Cerebellum;
 RC Fraser N.J.;
 RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
 RP TISSUE=Fetal brain;
 RX MEDLINE=20184290; PubMed=9933300;
 RA Peters H.C., Kaemmer G., Volz A., Kaupmann K., Ziegler A., Bettler B.,
 RA Epplen J.T., Sander T., Riess O.;
 RT "Mapping, genomic structure, and polymorphisms of the human GABAB1
 RT receptor gene: evaluation of its involvement in idiopathic
 RT generalized epilepsy.";
 RL Neurogenetics 2:47-54(1998).
 [8]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RP Younger R.;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RL [9]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP TISSUE=Cerebellum;
 RX MEDLINE=99108069; PubMed=9889352;
 RA Makoff A.;
 RT "Molecular cloning of human GABAB1 and its tissue distribution.";
 RL Brain Res. Mol. Brain Res. 64:137-140(1999).
 [10]
 RN SEQUENCE FROM N.A. (ISOFORM 1B).
 RP TISSUE=Prostate;
 RX MEDLINE=20493604; PubMed=10906333;
 RA Schwarz D.A., Barry G., Eliasof S.D., Petroski R.E., Conlon P.J.,
 RA Maki R.A.;
 RT "Characterization of gamma-aminobutyric acid receptor GABAB(1b), a
 RT GABAB(1) splice variant encoding a truncated receptor.";
 RL J. Biol. Chem. 275:32174-32181(2000).
 [11]
 RN VARIANTS VAL-20 AND SER-489.
 RX MEDLINE=99332163; PubMed=10402495;
 RA Sander T., Peters C., Kaemmer G., Samochowicz J., Zirra M.,
 RA Mischke D., Ziegler A., Kaupmann K., Bettler B., Epplen J.T.,
 RA Riess O.;
 RT "Association analysis of exonic variants of the gene encoding the

RT GABAB receptor and idiopathic generalized epilepsy.";
 RL Am. J. Med. Genet. 88:305-310(1999).
 [12]
 RN R1A-R2 INTERACTION.
 RP MEDLINE=20237752; PubMed=10773016;
 RX Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,
 RA Johnson M.P., Hebert T.E., Ethier N., Bellet M., Metters K.,
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
 RT receptors with truncated receptors and metabotropic glutamate
 RT receptor 4 supports the GABA(B) heterodimer as the functional
 RT receptor.";
 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
 [13]
 RN R1A-R2 INTERACTION.
 RP MEDLINE=99102694; PubMed=9872744;
 RX Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of heteromer formation in GABAB receptor function.";
 RL Science 283:74-77(1999).
 CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED
 CC BY PHACLOFEN.
 CC -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY
 CC OF FUNCTIONAL GABA-B-R1A/GABA-B-R2 HETERODIMERS BY COMPETING FOR
 CC GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT
 CC CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR
 CC CENTRAL VERSUS PERIPHERAL SITES.
 CC -!- COPACITOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS
 CC UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A (SHOWN HERE), 1B, 1C, 1D AND
 CC 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS
 CC CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE
 CC CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN
 CC ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF
 CC GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION
 CC BETWEEN ISOFORM 1A AND GABA-B-R2.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART,
 CC SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND
 CC MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM
 CC 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS
 CC KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE
 CC MARROW, THYMUS AND MAMMARY GLAND.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PRO0248; GPCRMR.
DR PRINTS: PRO1176; GABABRECEPTR.
DR PRINTS: PRO1177; GABAB1RECEPTR.
DR PRINTS: PRO1178; GABAB2RECEPTR.
DR PROSITE: PS0099; PRO_RICH; 1.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Postsynaptic membrane; Coiled coil; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 41
FT CHAIN 42 941
FT
FT DOMAIN 42 483
FT TRANSMEM 484 504
FT DOMAIN 505 522
FT TRANSMEM 523 543
FT DOMAIN 544 551
FT TRANSMEM 552 572
FT DOMAIN 573 597
FT TRANSMEM 598 618
FT DOMAIN 619 654
FT TRANSMEM 655 675
FT DOMAIN 676 691
FT TRANSMEM 692 712
FT DOMAIN 713 720
FT TRANSMEM 721 741
FT DOMAIN 742 941
FT
FT CARBOHYD 781 819
FT CARBOHYD 90 90
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FT CARBOHYD 404 404
FT CARBOHYD 453 453
FT VARSPLIC 902 927
FT VARSPLIC 929 941
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FT VARIANT 628 628
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FT VARIANT 869 869
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FT CONFLICT 6 6
FT CONFLICT 12 12
FT CONFLICT 424 424
FT
SQ SEQUENCE 941 AA; 105821 MW; 09F1773DB0673C5D CRC64;

Query Match 15.9%; Score 1066.5; DB 1; Length 941;
Best Local Similarity 29.5%; Pred.No. 6.3e-67;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;

QY 155 LLGLFELSTSRGPRDGLSELGAATMAVEHINKRLLPGYITLVLVNTDCTDPCGVGVDRF 214
DB 58 INGLPLTKEVAKSGTGRVLPFAVELAIEQIRNESLLRPYFLDLRLYDTECDNAKGLKAF 117
QY 215 FHAIYQTPSTRMVLGSCSEVTESLAKVVPVNNIVQVSFGTSFALSDDREFFPYRT 274
DB 118 YDAIKYGNP-HLMVPGGCVPSVTSIAESLQGNLVLQLSFAATTPVLADKKYPYFRT 175
QY 275 VAPDSHNPARTAFIRKFGWGVITTSQNEEHVSLAVNNLVLELANISCAATIFPA-- 332
DB 176 VESDNAVNPAILKLLKHQYQKRVGTLTQDVQRESEVRNLDLTGVLYGEDIEISDTESFSD 235
QY 333 -ATDFEQLLLRETDTRIIGSFCSDELAPQILCEAYRLRMFGADYAWILHESGAPWPP 391
DB 236 PCTSVKK-----LKGNDVRIILGQFDONMAAKVFCCAAYEENMYSKYOWIIPGWYEPSW 291

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QY 392 DORT-----ACSNHELOLAVENLIVVSTHNSIVGNVSVSGLNHNMFNSQLRKQSQAFHG 446
DB 292 QVHTEANSRCKRKNLLAAEGYI-----GVDFEPLSSKQIKTISGTPQOQYER 340
QY 447 Q-DGFGSGVGPRISTAAATQSDSRRRRRRGVGTSGGHLFPEAISQVAPOTYDAVWAIALA 505
DB 341 EYNNKRSVGVP-----SKFHGVAYDGIWVIAT 368
QY 506 LRAAEHRRNEEQSKLDFDYTRSDMAWEFLQOMGKLHFLGVSGVPSFGDRVGTTF 565
DB 369 LQRAMETLHASSRHQIQDFNVDHTLGRILNAMNETNFFGVGTGVVFRNGERMGTIKF 428
QY 566 YQIQGILLEPVVALYPATDPRCPRCPRVKHWSQVPIAKRVFKLKVATTAPAFYTI 625
DB 429 TQFODSRVKKVGEYNAVADTLEIIND---TIRFQSGEPKPKDKTIILEQLRKISLPLYSIL 485
QY 626 ATLSVSGIALATFTEAFNLHFRKAKLSPKLSNITAVGCFIVYATVILLGLDHSITLP 685
DB 486 SALTILGIMIMASAFFNKKRNQKLIMSSPYMNNLIILGGMLSYASIFLFLDGSFV- 544
QY 686 SAEDSFATVCTARVYLLSAGFSLAFSGMFAKTYRVHRIFRTGVSFKDKMLQDIQILILV 745
DB 545 -SEKTFELCTVTRWILTVGYTTAFGAMFAKTRVHAIEKNV--KMKKKIISKQKLLVIV 601
QY 746 GGLLVLDALLVTVVTPDPMERHLNLTLEISATRSVYVQPOVEVCRSQHTQWLSVLY 805
DB 602 GGMLLIDILICLWQAVDPLRRTVEKYSMEPDPAGRDISIRPLLEHCENTHMTIWLGIYV 661
QY 806 AYKGLLVGVVMAWETRHVKIPALNDSQYIGVSVSVVITSIVVLANLISERVTLAF 865
DB 662 AYKGLLMLFGCLAWETRNVSIIPALNDSKYIGMSVYVNGIMCIIGAAVSFLTRDQPNVOF 721
QY 866 ITITALITSTATLCLLFPKLHDIWARNDIIDPVHSMGLKMECNTRFRVVDORREILQ 925
DB 722 CIVALVIFVCSITILCLVFPKL-----ITLRTNPDAQTNRREQ 761
QY 926 YRVEQNVYKKEIQALDAEIRKLERLLESGLTTSTTT--SSSTSLLTG-----GGHLKP 979
DB 762 F---TQNG--KK-----EDSKTSTSVTSVNOASTSRLEGLQSENHRLRM 800
QY 980 ELT-----VTSGISOTPAASK-----NRTPSISG---ILPNLLLS 1011
DB 801 KITELDKLEEVTMOLOQDTPEKTYIKONHYOELNDILNLGNFTSTEDGGKAILKNHL-- 858
QY 1012 VLPPVIPRASWPSAE 1026
DB 859 ---DONPOLWNTE 870
RESULT 3
GBR1_HUMAN
ID GBR1_HUMAN STANDARD; PRT: 961 AA
AC Q9UBS5; Q95375; Q9UCQ0; Q96022; Q95975; Q95468;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GB1).
GN GABBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Cerebellum;
RX MEDLINE=99061981; PubMed=9844003;
RA Kaupmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H.,
RA Heid J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
RT expressed and regulate inwardly rectifying K+ channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [2]

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Db 761 F---TQNO--KK-----EDSKTSTSVTSVQNSRLEGLQSENHRLRM 799
QY 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011
Db 800 KITELDKLEEVTLQLODTPKTYIKQNHQYELNDILSLGNFTSTGGRAILKNHL-- 857
QY 1012 VLPVPVPRASWPSAE 1026
Db 858 ---DQNPQLQWNTTE 869
RESULT 2
GBR2_HUMAN
ID GBR2_HUMAN STANDARD; PRT; 941 AA.
OC 075999; 075974; 075975; 09UN59; Q9UNR1; Q9P1R2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR
DE 51) (GPR 51) (HG20).
GN GABBR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor";
RL Nature 396:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCreia K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Petal brain;
RX MEDLINE=99189236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface

expression and coupling to adenylyl cyclase in the absence of
GABABR1."; Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RP R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
RT functional GABAB receptor activity."; J. Biol. Chem. 274:7607-7610(1999).
RN [8]
RP R1A-R2 INTERACTION.
RX MEDLINE=2037752; PubMed=10773016;
RA Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RT receptor."; J. Pharmacol. Exp. Ther. 293:460-467(2000).
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CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----
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CC -----
CC EMBL; AJ012188; CAA09942.1; -
CC EMBL; AF056085; AAC63228.1; -
CC EMBL; AF095723; AAC63383.1; -
CC EMBL; AF095724; AAC63384.1; -
CC EMBL; AF095784; AAC30389.1; -
CC EMBL; AF074483; AAD03336.1; -
CC EMBL; AF069755; AAC99345.1; -
CC EMBL; AF099033; AAD45867.1; -

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:08:01 ; Search time 24.07 Seconds
(without alignments)
1987.852 Million cell updates/sec

Title: us-09-715-962-6

Perfect score: 6705

Sequence: 1 MRLIQPVQTRYGPWPAVGL.....RLSLGDSQEEEQAPANGTE 1305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1068.5	15.9	940	1 GBR2_RAT	O88871 rattus norv
2	1066.5	15.9	941	1 GBR2_HUMAN	O75899 homo sapien
3	991.5	14.8	961	1 GBR1_HUMAN	Q9ubss5 homo sapien
4	990.5	14.8	960	1 GBR1_MOUSE	Q9wv18 mus musculu
5	971.5	14.5	991	1 GBR1_RAT	O920u4 rattus norv
6	372	5.5	877	1 MGR6_HUMAN	O15303 homo sapien
7	367	5.5	871	1 MGR6_RAT	P33349 rattus norv
8	349.5	5.2	872	1 MGR2_HUMAN	Q14416 homo sapien
9	349.5	5.2	915	1 MGR7_HUMAN	Q14831 homo sapien
10	348.5	5.2	915	1 MGR7_RAT	P35400 rattus norv
11	347	5.2	912	1 MGR4_HUMAN	Q14833 homo sapien
12	343.5	5.1	872	1 MGR2_RAT	P31421 rattus norv
13	343	5.1	879	1 MGR3_RAT	P31422 rattus norv
14	339.5	5.1	908	1 MGR8_RAT	P70579 rattus norv
15	337.5	5.0	908	1 MGR8_HUMAN	O00222 homo sapien
16	336.5	5.0	908	1 MGR8_MOUSE	P47743 mus musculu
17	336	5.0	912	1 MGR4_RAT	P31423 rattus norv
18	320	4.8	877	1 MGR3_HUMAN	Q14832 homo sapien
19	306.5	4.6	976	1 MGR_DROME	P91685 drosophila
20	306.5	4.6	999	1 MGR1_CAEEL	Q09630 caenorhabdi
21	257.5	3.8	1199	1 MGR1_RAT	P23385 rattus norv
22	257	3.8	1203	1 MGR5_RAT	P31424 rattus norv
23	242	3.6	1194	1 MGR1_HUMAN	Q13255 homo sapien
24	240	3.6	1085	1 CASR_BOVIN	P35384 bos taurus
25	237	3.5	1078	1 CASR_HUMAN	P41180 homo sapien
26	230.5	3.4	1079	1 CASR_MOUSE	Q9gy96 mus musculu
27	223.5	3.3	1212	1 MGR5_MOUSE	P41594 homo sapien
28	221.5	3.3	1079	1 CASR_HUMAN	P48442 rattus norv
29	166.5	2.5	1047	1 ANPB_BOVIN	P46197 bos taurus
30	166.5	2.5	1047	1 ANPB_RAT	P16067 rattus norv
31	162.5	2.4	1047	1 ANPB_HUMAN	P20594 homo sapien
32	160	2.4	847	1 .MMLB_STRCO	O54101 streptomyce
33	137	2.0	369	1 LIVK_ECOLI	P04816 escherichia

RESULT 1

ID	GBR2_RAT	STANDARD;	PRT;	940 AA.
AC	O88871; Q9QWU2; Q9JK36;			
DT	20-AUG-2001 (Rel. 40, Created)			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).			
GN	GABBR2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Chordata; Sclurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hypothalamus;			
RX	MEDLINE=99087320; PubMed=9872315;			
RA	Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,			
RA	Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,			
RA	Salon J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,			
RA	Branchek T.A., Gerald C.;			
RT	"GABA(B) receptors function as a heteromeric assembly of the subunits			
RT	GABA(B)RI and GABA(B)R2.";			
RL	Nature 396:674-679(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain cortex, and Cerebellum;			
RX	MEDLINE=99087322; PubMed=9872317;			
RA	Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,			
RA	Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,			
RT	Bettler B.;			
RT	"GABA-B receptor subtypes assemble into functional heteromeric			
RL	complexes.";			
RL	Nature 396:683-687(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain cortex;			
RX	MEDLINE=20193514; PubMed=10727622;			
RA	Clark J.A., Mezey E., Lam A.S., Bonner T.I.;			
RT	"Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";			
RL	Brain Res. 860:41-52(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hypothalamus;			
RA	Borowsky B., Laz T., Gerald C.;			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.			
RC	TISSUE=Hippocampus;			
RX	MEDLINE=99102694; PubMed=9872744;			
RA	Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,			
RA	Kornau H.-C.;			
RT	"Role of Heteromer Formation in GABA-B Receptor Function.";			
RL	Science 283:74-77(1999).			
CC	-I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS			

34	133.5	2.0	369	1	LIVK_SALTY	P17216 salmonella
35	133	2.0	537	1	ANPC_BOVIN	P10730 bos taurus
36	132.5	2.0	1687	1	VIT2_FUNHE	Q98893 fundulus he
37	131.5	2.0	540	1	ANPC_HUMAN	P17342 homo sapien
38	130.5	1.9	536	1	ANPC_MOUSE	P70180 mus musculu
39	130.5	1.9	722	1	HMN2_DROME	P22808 drosophila
40	127	1.9	821	1	ALG1_HUMAN	O43747 homo sapien
41	125.5	1.9	2300	1	CYAA_NEUCR	Q01631 neurospora
42	123.5	1.8	1113	1	HDA5_MOUSE	Q92246 mus musculu
43	122.5	1.8	2167	1	BEM2_YEAST	P39960 saccharomyc
44	122	1.8	535	1	ANPC_RAT	P41740 rattus norv
45	121.5	1.8	565	1	SCRI_SCHPO	O14335 schizosacch

ALIGNMENTS

```

DE F45H11.4 PROTEIN.
GN F45H11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RA Kelly P.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150716; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smalton N., Smith A., Sonnenhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA McMurray A.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z78420; CAB01711.1; -.
DR EMBL; Z78418; CAB01711.1; JOINED.
DR EMBL; Z78418; CAB01699.1; -.
DR EMBL; Z78420; CAB01699.1; JOINED.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR001871; bZIP.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PROSITE; PS02529; G_PROTEIN_RECEP_F3_4; 1.
DR SMART; SM00338; BRL2; 1.
SQ SEQUENCE 1267 AA; 142175 MW; 7820C36287FB2428 CRC64;

Query Match          4.2%;   Score 283.5;   DB 5;   Length 1267;
Best Local Similarity 19.9%;   Pred No. 5,6e-12;
Matches 273; Conservative 198; Mismatches 508; Indels 393; Gaps 64;

Qy 136 ESERMSPAEMORNGKIVLGLFEL-----STSRGP--RPDGLSELGAATMAVEHINR 187
   : || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 23 QQSARMLVAEI---HGEIQIGALFPIHROIAGSESCGEIWEQVGIQRSEIAMLTVKOLNE 79
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 188 KRLLPGYTLLELVNTDT-----QCD-----PGVGVDRFFHAIYTOPS 223
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 80 E--LP-FKLGLSIRDSWTERIAMEQTIAFLREGVAQSCCOTPGC-----NKKs 126
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 224 TRVMVLGASACVEVTESLAKVYNNIVGVSGFSGSPALSDRREFFYFVRTVAPDSSHP 283
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 127 VPVAVIGPGKSSSIIVANVLQVRIPOVGYSAITPDLSDKEQFGYFLRVPSDFVQAO 186
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 284 ARIAFIRKFGWGTVTTFSONEEVHSLAVNNLVTELEAANISCAATITFAATDFKEQLLLL 343
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 187 AINRLLHHYNTYVAVLYSAGNYGKGPESL--EKLIHRSSSVCIAYSE---KIRTLAS 241
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 344 RETDTRIIGFSQELAPQIL---CEAYRLRMFG-----AD-----YAWITLHSMGA 387
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 242 EOEYRQVLTRLDSQNSRPQVYVCFEGASMRMFFFAQKHLADGKMQMKRFQWI-----GS 296
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 388 PWWPQRTACSNHQLQAVENLIVVSTH--NSIVGNVSYSGLN--NHMFNSQLR-----K 439
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 297 DGWADRNDV--EDLEEEAGSFSIRIHAPKIPGFRQYITALHPENMTNPNWFRFQWQK 354
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 440 QSAOPHGODGFGSGYGPRIISAATQSDSRRRRRRVGVGTSGGHLFPEAISQY-----APQ 494

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Search completed: April 30, 2002, 10:07:49
Job time: 421 sec

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Db 355 FNCQF-----AVSKED---KNNENIRICSDENLDE---QYKEDPKLSQ 392
   : || : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 495 TYDAVMAIALALRAA--EHWRRNEEQSKLDFDTRSDMAWEFLQOMGKL---HFLVSG 550
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 393 VINSIRVVALGLKAMYQDRCDN-----STLCTEMLSRNGLLLEYLLNVTY 439
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 551 PVFSFGP---DRVG--TTAFYQI-----QRGLLEPV-----ALY 579
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 440 SDQFKQPVYFDRNGDPPAWYDILNVIGTKDLNDPNEYVSEFKSINDYGVLEDMTAKSMF 499
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 580 YPATDALD-----FRPCRCRPVKWHS-----GOVPTAK 607
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 500 FDKTELLPESVCSRPGIGIQORETMACWCICESCLDIQYVKNKTTNOCMNCTLGSWPNAN 559
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 608 RV-----FKLRVATIAPLAFYTIATLSSVGLALATIFLAFNLHFRKKAIKLSSPKLSNIT 663
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 560 RTGCEYIPEVSWTSFGHIALVLAVTGITSTMATLAVLRHNSTPVVKSTRELSYII 619
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 664 AVGCIFYVATVILLGLDHSITLPSAEDSPATVCTARVYLLSAGFSLAFGSMFAKTVRHRI 723
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 620 LSGLVACYAVSFALLATPST-----TSCFITRVIPPIAFVAVVYSALLTKTNRIARI 670
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 724 FTRTGS-----VFKDKMLQDILILLVGLLLVDALLVTLVWVDDPMERHLNHLFLEISA 778
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 671 L--AGSKKRILTKKPRFLTTFEQVITWILVAVOCVIVGVGLMRD-----WPDATYAKYA 723
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 779 TDRSVYQPOVEVCRSOHTOWLSVLYAYKGLLVGVVYMAWETHRVHKIPALNDSQYIGV 838
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 724 LPRKLIILECDTE-----TKSFL-IPFFWDFFLTCTLYAFKTRNLP-ENFNEAKIGF 775
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 839 SVYS-----VVITSIVVVLANLISERVTLAFI-----TITALILT-----S 875
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 776 TISOPAKSLPFQKEHVIIFOYCTV-----VWIAFLVLHMGTTTHKALVMSFSYLS 827
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 876 TTAFLCLLTPKLDHIWARNDIIDPVHSMGLKMECNTRFRVVDRLQYRVEYONRVY 935
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 828 ASVALALLFPKLYII-----LMHP-----EKNIR-----ASYTTTKLIRCH 864
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 936 KKEQALDAEIRKLERLLESGLTSTTTT---SSSTSLTTGGGHLKP---ELTVTSGIS 988
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 865 FGNSQAAVDSTSKOHL---GSKTTARTSVQSGSASKSSMGGVVTRTASVHPVSRGST 921
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Qy 989 QTPAASKNRTPSISGILPNLLSVL---PPVIPRASWPSAEYMQIPMRRSVTFASQPOL 1044
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 922 HSTDVSTQTEGLRSIFPLIMFKIVFLSNFDILLAASKFSRFSIVGRKKQGLDDVQOL 981
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 1045 EEACLPAD--LINLRKAH--QOATEAKTGLI-----NRLRGIFSRITSSNKG----- 1088
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 982 VDACCRRYODEKINSAAANLLESEDEVGALLADSIENSMRTVLS--TVAGKAVVPLVPM 1039
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 1089 -----STASLADOKGLKAAFKSHMGL-----FTRLIPSSOTASCNAINNN 1128
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Db 1040 VPMIPVVTLPAPSOEDNFEQAGFEKCOLSKDLSRKSPKQFLHVPKSRCTSRV--- 1096
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 1129 PNQDSIPSEASSHP--NGNHLKPIHRGSLITKSG-----THLDHLTKDPNFLDPIPTIS 1178
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1097 -----SSYTIMSGNQQLMSPMGVSSAGSGSPWSSFDHLSDE-----ELAQIS 1142
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Qy 1179 GGEQGDOTLG-----GKYVKLLETKVNFQPLSNRRRPSVVO--QPPSL 1218
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1143 VRQLNQKLMGDRNVVMQWKRRRLTKNRGYALNCRARRVNNOVQLEADNMLNRQIKTL 1202
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Qy 1219 RERVGS-----PRF-----PHRILPPTCSLALAESEDRPGDSTS 1254
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 1203 REALSEAOMLHYEPVFYQAYPSIVPSTTSPVTVSLPTIARPIPVPPDSTA 1254
   : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

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QY 448 DG-----FGSGYGRPRISIAATQSDSRRRRRGVGTSGHLPFAISQYAPQTYDA 498
Db 448 KGADSIKFDYGDGMG-RYNVNFQHHGGKSYLYK-----GH-----485
QY 499 VWATALARAEEHWRNEQSKLDGFDYTRSDMAWEFLQMGKHLFLGVSPVSGPDD 558
Db 486 -WAETLYLDVDSIHWSR-----SVPTS-QCSD 511
QY 559 RVGTFAYQIORG-----LLEPVALYYPATDADFRCPRCPVKWH-----SGQVPYAKRV 609
Db 512 PCAPNEMKNQPGDVCCVICPCEPEYLVLD--EFTCMDCGPGQWPTADLSGCYNLPEDY 569
QY 610 FKLRA-TIAPLAFTIATLTVSGTALAIT-FLAFLNHLFRKKA IKLSPKLSNITAVGC 667
Db 570 IRWEDAWAIGPV---TIACLGFMCTCIVITVFIKH-----NPLVKASGRELICYILLFGV 622
QY 668 IFVYATVILLGLDHTLPSAEDSFATCTARVYLLSAGFSLAFSGMFAKTYRVHRIF--T 725
Db 623 SLSCYMTFFF-----IAKFS-----PVICALRRLGLGTSPAICYSLTNTNCIARIFDGV 673
QY 726 RTGSYFKDKMLQDIOILILVGLLLVDALLVTLWVTDPMERHLNHLTLEISATDRSVY 785
Db 674 KNGAQ-RPKFISPSQVFCICGLILVQIMVSVWLI-----LETPGTRYTLTP 720
QY 786 QPOVEV-----CRSQHTQTLWLVLYAYKGLLVGVYMAWETRVHKVIPA-LNDSQYIGSVY 841
Db 721 EKRETVILKCNVKDSMLISL--TYDVLVILCTVYAFKTR--KCPENFNKAFIGFTMY 776
QY 842 SVWITSATVVVLANLISERVTLAFITITILITST-----TATLCL-----LF 884
Db 777 TTCI-----IWLAFLPI--FYVTSSDYRVQTTTMCISVLSGFWVLGCCLF 819
QY 885 IPKLHDIWARNDIIDPVHSMGLKMECNTRFVWDRLRELQYRVEQNVKKEIQALDA 944
Db 820 APKVHIV-----LFQP-----QKNV-VYHRLH-----840
QY 945 EIRKLERLESGLTTTSTTSTSTSLT 972
Db 841 ----LNRFVSVSGTATTYSQSSASTYVPT 864

RESULT 13
Q9PWE1 ID Q9PWE1 PRELIMINARY; PRT; 977 AA.
AC Q9PWE1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR (FRAGMENT).
GN GLUR.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Hellmich H.L., Micci A.M., Sanchez X., Christensen B.N.;
RT "Molecular cloning, functional expression and localization of a novel
RT metabotropic glutamate receptor linked to calcium mobilization from
RL the catfish retina."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076473; AAD47893.1;
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF01094; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS02529; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
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FT NON_TER 977 977
SQ SEQUENCE 977 AA; 108759 MW; BD06A67E240751CE CRC64;

Query Match 4.6%; Score 311.5; DB 13; Length 977;
Best Local Similarity 20.7%; Pred. No. 3.1e-14;
Matches 181; Conservative 129; Mismatches 342; Indels 221; Gaps 33;

QY 141 MSPAEMORNH-----GKIVLLGLFELSTSRGP-----RPGDLSLGAATMAV 182
Db 38 VSPALMAHQHTPHSIKIPGDVTLGGLFPVH-SKGPLGQACGEIKKEKGVHRMEAMLYAL 96
QY 183 EHINR-KRLPLGYTL-----ELVTNDQCPDGPVGVDRRF 215
Db 97 DQINSDPELLPNITRLDTCSDRTYALQSLTFVQALIKQKDTSDIRCSNGE-----150
QY 216 HAIYTOPSTRMVLMLGSACSEVTESLAKVVPWNIVQVSFGSTSPALSDREFFPYFTV 275
Db 151 OPTIRKPE-RVGVIGASASSVIMVANVLRFLFPIQISYASTAPELSDNNRNYDFSrv 209
QY 276 APSSSHNPARIATIRKFGWGTVTTFQSENEVHSLAVNNLV-TELEAANIISCAATITFAAT 334
Db 210 PPSYQQAQAMVDIVKALGNVYFIIASGNYGESGVDAFVQISREAGGLCAQSMKIPRD 269
QY 335 ----DFKEQLLLRLRET-DTRIIIGSFQELAPQILCEAYLRMFGADYAMILHESMGAPW 389
Db 270 PKPGEFKIIKRLMETPNARGIIIFANEDDIKQVLEAARRANLTG-HFKFVGSWSGAKS 328
QY 390 WPDQRTACSNHELQLAIVENLIVSTHNSIVGNVNSYSGLNNHMFNSQLRKQSAQFHGQDG 449
Db 329 AP-----ILDNEEVAEGAVTILPKRASVEGFDQYFTRSRLENRRNRNITWFAEF 375
QY 450 FGSYGGRPRISIAATQSDSRRRRRGVGTSGHLPFAISQYAPO-----TYDAYVA 501
Db 376 WEDDFCKLTTPG-IKLDPEKKKCTG-----KERIGRSPYEQBGKQVQVIDAYVA 425
QY 502 IALARAEEHWRNE-----EQSKLDG--FDYTRSDMAWEFLQMG-----541
Db 426 MAHALHNNHQTCARGRTLCRMDPVEGRLLLSYIR---AVNFNGSAGTGVLFNENGAPG 482
QY 542 ----KLHFLGVSGP-----VSFGPDRVGTTFAYQI-----QRGLLEPAL-----578
Db 483 RYDIFYQFSNTSPGYKVIQGSFSSIAKTSPPGYKVFQGWNTNLGINEVEEMQSGGE 542
QY 579 -YYPATDALDFRC--PRCRPVK-----WHS-----GOVPIAKRVFKLRVATIAP 619
Db 543 HYIPAS-VCSPFCQPGERKKMVKGVPCWCHCEPCDGYQYQVGGELTCEMCPDMR-----P 596
QY 620 LAFYTIAT-----LSSVGIALAITFLAFNLHFRKLKAIKLSPKLS 660
Db 597 TANHTACTPTPIIKLDWHSNPAVPMFLAILGIAATLSVIVFVFNDDTPIVRASGRELS 656
QY 661 NITAVGCIFFVYATVILLGLDHTLPSAEDSFATCTARVYLLSAGFSLAFSGMFAKTYRV 720
Db 657 YVLLTGIFLIYLIITFLMTAEPNTV-----VCALRRLGLLGMCITYSAMLTKTNR 707
QY 721 HRIFT-TGSVFKDKMLQDIOILILVGLLLVDALLVTLWVTDPMERHLNHLTLEISAT 779
Db 708 YRIFEQGGKSTAPKFIPTSQLVITFILVDFQVIGVFIWFGVVPDH-----TIV 757
QY 780 DRVVYQPOVEVCRS---OHTQTLWLVLYAYKGLLVGVYMAWETRVHKVIPALNDSQY 835
Db 758 DYDELRPNPPELARGILKCDMSDLSLICLSYSILLWVCTVYAVKSGVP-ETFNKAP 816
QY 836 IGVSYSVWITSATVVVLANLISERVTLAFITI 868
Db 817 IGFTMYTTCI-----VWLAFAVPI 834

RESULT 14
Q9V485 ID Q9V485 PRELIMINARY; PRT; 976 AA.
AC Q9V485;
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DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.
DR PROSITE; PS02059; G_PROTEIN_RECEPT_F3_4; 1.
DR SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Query Match 5.0%; Score 336; DB 11; Length 983;
Best Local Similarity 22.1%; Pred. No. 4.7e-16;
Matches 193; Conservative 134; Mismatches 346; Indels 200; Gaps 36;

QY 148 RHNGKIVLGLPELSTSRG-----PRDGLSELGAATMAVEHINR-KRLLPQVYLE 197
D 148 RHNGKIVLGLPELSTSRG-----PRDGLSELGAATMAVEHINR-KRLLPQVYLE 197
D 44 RIDGDITLGLLFPVH-GRSGEKGACGELKKEGTHRLLEAMLFALDRINNDPDLNITLG 102
QY 198 LVTNDPQCDPGVGVDRFFHA-----LYTOPSTRMVMALL 230
D 198 LVTNDPQCDPGVGVDRFFHA-----LYTOPSTRMVMALL 230
D 103 ARILDT-----CSRDTHALEQSLTFVRALIEKDGTEVRCGGGPPITKPE-RVGVGI 154
QY 231 GSACSEVTESLAKVVPWNIVQVSGSTSPALSDRRREFPYFRTVAPDSSHNPARIAFIR 290
D 231 GSACSEVTESLAKVVPWNIVQVSGSTSPALSDRRREFPYFRTVAPDSSHNPARIAFIR 290
D 155 GASGSSVSIWVANILRLFKIPIQISYASTADLSDNSRYDFEVSVPDSTYQAQAMVDIVR 214
QY 291 KFGWGVTFTTSONEEVHSLAVNNLVTE-LEAANISCAATITF-----AATDFKEQLLLRE 345
D 291 KFGWGVTFTTSONEEVHSLAVNNLVTE-LEAANISCAATITF-----AATDFKEQLLLRE 345
D 215 ALKNWVSTLASGYSGESGVEAFIQKSRENGVCIAQSVKIPREPKTGEFKIIRLLE 274
QY 346 TDTRIIIGSFQELAPQILCEAVLRMFGADYAWILHESGAPWPPORTACSNHEQLQLA 405
D 346 TDTRIIIGSFQELAPQILCEAVLRMFGADYAWILHESGAPWPPORTACSNHEQLQLA 405
D 275 TSNARIGIIFANEDDIRRVLEAARRANQTGHFFWMSDSWGSKSAPVLR-----LEE 327
QY 406 VENLIVVSTHNSIVGNVSVGLNNHMFNSOLRKSQAQFHGQDGFSGYGRISAIATQS 465
D 406 VENLIVVSTHNSIVGNVSVGLNNHMFNSOLRKSQAQFHGQDGFSGYGRISAIATQS 465
D 328 AEGV-----TILPREMSVGRDFRFSSTLDNRRNIWFAEFWDNFCKLSRHALKK 381
QY 466 DSRRRR--RGVVGTSGGHLFPALISQYAPQTYDAVMAIALRAAEHVN--RRNEQSK 521
D 466 DSRRRR--RGVVGTSGGHLFPALISQYAPQTYDAVMAIALRAAEHVN--RRNEQSK 521
D 382 GSHIKKCTNRERIGQDSAY-EQEGKQVF---VIDAVYAMGHALHAMHRDLCPGRVGLCP 437
QY 522 LDGFDYTRSDMAWEFLQMGKHLFLVSG-PVSFS-GPDVRGTAFYQIQRGLLEPVLY 579
D 522 LDGFDYTRSDMAWEFLQMGKHLFLVSG-PVSFS-GPDVRGTAFYQIQRGLLEPVLY 579
D 438 MDPVDGT-----QLLKIRNWNFSGIAGNPVTNENGAPGRYDIYQYQ---LRNGSAE 488
QY 580 YPA---TDALDFRCPR-----CRP-----VK-----WH----- 599
D 580 YPA---TDALDFRCPR-----CRP-----VK-----WH----- 599
D 489 YKVGISWTDLHLRIERMQWPGSGQQLPRISICSLPCQGERKKTVKMACCNHCEPCTGY 548
QY 600 -----SQGVPIAKRVFKLRVATIAPLAFYTTIATLSSVGIA- 634
D 600 -----SQGVPIAKRVFKLRVATIAPLAFYTTIATLSSVGIA- 634
D 549 QYQVDRYTCKTCPYDMRPTENRTSCQPIPIVKLEWDSWA-VLPL-----FLAVVGIAA 601
QY 635 ---LAITFLAFNLHFKLKAIKLSFKLSNITAVGCIFFVATVILLGLDHTLPSAEDSF 691
D 635 ---LAITFLAFNLHFKLKAIKLSFKLSNITAVGCIFFVATVILLGLDHTLPSAEDSF 691
D 602 TLFVVVTFRYN---DTPIVKASGRELVSLLAGIFLCYATFLM-----IAEPDL 649
QY 692 ATVCATRVLLSAGSFLAFSGFAKRYVHRIFTR-TGSVFEDKMLQDIOILLVGLLL 750
D 692 ATVCATRVLLSAGSFLAFSGFAKRYVHRIFTR-TGSVFEDKMLQDIOILLVGLLL 750
D 650 GT-CSLRRIFLGLGWSISYAALLTKNRIYRIFEQKRSVSAPRFISPASQLAITFLIS 708
QY 751 VDALLVTLWVTDPMERHLNLTLEISATDRSVV-YQQVQE-----YCRSQHTOTWL 801
D 751 VDALLVTLWVTDPMERHLNLTLEISATDRSVV-YQQVQE-----YCRSQHTOTWL 801
D 709 LQLLGCYWFVVDP-----SHSVVDQDQRTDLPFRARGVLYKCDISL 753
QY 802 SVLYAKGGLLVGVVYMAWETHRVKIPALNDSQYIGVSVSV-VITSIAVVVL--ANLIS 858
D 802 SVLYAKGGLLVGVVYMAWETHRVKIPALNDSQYIGVSVSV-VITSIAVVVL--ANLIS 858
D 754 ICLLYSMLLMTVCTVYAIKTRGP-ETNEAKPIGFTMYTTCIVMLAFIPIFFGTSQA 812
QY 859 ERVTLAFITITAILITSTATLCLLPIPKLHDI 891
D 859 ERVTLAFITITAILITSTATLCLLPIPKLHDI 891
D 813 DKLYIQTTTLTVSVLSLSASVSLGMLYMPKVYII 845
```

RESULT 12

Q9QYS2

AC Q9QYS2

DT 01-MAY-2000 (TRENBLREL. 13, Created)

DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)

DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.

GN GRM3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV.

RX MEDLINE=20012997; PubMed=10544282;

RA Minoshima T., Nakanishi S.;

RT "Structural organization of the mouse metabotropic glutamate receptor

RT subtype 3 and its regulation by growth factors in cultured cortical

RT astrocytes.";

RL J. Biochem. 126:889-896(1999).

DR EMBL; AF170701; AAF06741.1; -.

DR EMBL; AF170697; AAF06741.1; JOINED.

DR EMBL; AF170698; AAF06741.1; JOINED.

DR EMBL; AF170699; AAF06741.1; JOINED.

DR EMBL; AF170700; AAF06741.1; JOINED.

DR InterPro; IPR000337; GPCR_Mgr.

DR InterPro; IPR001828; ANF_receptor.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCR_MGR.

DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.

DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.

DR PROSITE; PS02059; G_PROTEIN_RECEPT_F3_4; 1.

DR Receptor.

KW Receptor.

'SQ SEQUENCE 879 AA; 99113 MW; F3A8B26CE96679EF CRC64;

Query Match 4.9%; Score 329; DB 11; Length 879;

Best Local Similarity 19.9%; Pred. No. 1.3e-15;

Matches 197; Conservative 133; Mismatches 332; Indels 326; Gaps 44;

QY 151 GKIVLLGLFELS-----TSRGRPDGLSELGAATMAVEHINRKR-LLPG-----YTL 196

D 151 GKIVLLGLFELS-----TSRGRPDGLSELGAATMAVEHINRKR-LLPG-----YTL 196

D 37 GDLVLGLGFPINEKGTGTECRINEDRGIQRLAEMLFADINKDNYLLPGVKLGVLHIL 96

QY 197 ELVINDT-----QCDPGVGVDRFFHAIYTPSTRMVLIGSAC 234

D 197 ELVINDT-----QCDPGVGVDRFFHAIYTPSTRMVLIGSAC 234

D 97 DTCSDTYALEQSLFVVRASLTKVDEAYMCPDG-----SYAIQENIPILLIAGVIGSY 150

QY 235 SEVTESLAKVVPWNIVQVSGSTSPALSDRRREFPYFRTVAPDSSHNPARIAFIRKFW 294

D 235 SEVTESLAKVVPWNIVQVSGSTSPALSDRRREFPYFRTVAPDSSHNPARIAFIRKFW 294

D 151 SSVSIQVALLRFLQIPQISYASTSAKLSKSDRYDFARTVPPDFYQAKAMAEILRYFNW 210

QY 295 GTVITFSQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKEQL-----LLLRETDPR 349

D 295 GTVITFSQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKEQL-----LLLRETDPR 349

D 211 TVSTVASEGDTGTEGFAEQEARLNICIAETAEKVGSRNIRKSYDSVIRELLQPNAR 270

QY 350 IIGSFSQELAPQILCEAVLRMFGADYAWILHESMGA----- 387

D 350 IIGSFSQELAPQILCEAVLRMFGADYAWILHESMGA----- 387

D 271 VVVLFRMSDDRELIAAASRV---NASFTWASDCWGAGQESIVKGSEHVAYCAITELAS 327

QY 388 -----QRTACS-----NH-----ELQLAYE----- 407

D 388 -----QRTACS-----NH-----ELQLAYE----- 407

D 328 HPVRFQDFRYFQSLNPNYNNHRNPFRDFWEQKFCQSLQNKRNHRQICDKHLAIDSSNYEQE 387

QY 408 -----NLIVVSTH-----NSIVGNVSVSGLNNHMFNSOLRKO-----SAQFHQ 447

D 408 -----NLIVVSTH-----NSIVGNVSVSGLNNHMFNSOLRKO-----SAQFHQ 447

D 388 SKIMEFVNNAVYAMAHALKMORTLCPTNTTKCDAMKILDKGKLYDKLLKINFTAPFPN 447

Query Match 99.5%; Score 6671; DB 5; Length 1305; Best Local Similarity 99.5%; Pred. No. 0; Matches 1299; Conservative 1; Mismatches 5; Indels 0; Gaps 0;									
QY	1	MRIQPVGTRYGMPAVGLRVLVLAALAWATSAAAWESSAEALQALGHEAIRPGAAISITS	60						
Db	1	MRIQPVGTRYGMPAVGLRVLVLAALAWATSAAAWESSAEALQALGHEAIRPGAAISITS	60						
QY	61	SPSSPPGESASTVTAGTTPIPRSDWKYKRTKVRRQQLNSHSLPGSTNASHAHLL	120						
Db	61	SPSSPPGESASTVTAGTTPIPRSDWKYKRTKVRRQQLNSHSLPGSTNASHAHLL	120						
QY	121	NLPPRQRYLKVNOVFESERRMSPAEMQRNHGKIVLGLFELSTSRGPRPDGLSELGAATM	180						
Db	121	NLPPRQRYLKVNOVFESERRMSPAEMQRNHGKIVLGLFELSTSRGPRPDGLSELGAATM	180						
QY	181	AVEHINRRLLPGYTLVNTQCDPGVGVDRFFHAIYTOPSTRMVMLLGSACSEVTES	240						
Db	181	AVEHINRRLLPGYTLVNTQCDPGVGVDRFFHAIYTOPSTRMVMLLGSACSEVTES	240						
QY	241	LAKVVPYNNIVQVSFGSTSPALSDRREFFPYFYRTVAPDSSHNPARIATIRKFGWGVTTF	300						
Db	241	LAKVVPYNNIVQVSFGSTSPALSDRREFFPYFYRTVAPDSSHNPARIATIRKFGWGVTTF	300						
QY	301	SONEVHSLAVNNLVTELEAANISCAATTFAATDPKEQLLLRETDTRIIGSFQOELA	360						
Db	301	SONEVHSLAVNNLVTELEAANISCAATTFAATDPKEQLLLRETDTRIIGSFQOELA	360						
QY	361	PQILCEAYRLRMFGADYAWILHESGAPWMPQORTACSNHEQLQAVENLIVVTHNSIVG	420						
Db	361	PQILCEAYRLRMFGADYAWILHESGAPWMPQORTACSNHEQLQAVENLIVVTHNSIVG	420						
QY	421	NNVSYGLNNHMFNSQLRKQSAQFHQDGFSGYGRISIAATQSDSRRRRRGVGTSG	480						
Db	421	NNVSYGLNNHMFNSQLRKQSAQFHQDGFSGYGRISIAATQSDSRRRRRGVGTSG	480						
QY	481	GHLFPEATISQVAPQTYDVAWAIALARAAEHWRRNEEQSKLDGFDYTRSDMAWEFLQOM	540						
Db	481	GHLFPEATISQVAPQTYDVAWAIALARAAEHWRRNEEQSKLDGFDYTRSDMAWEFLQOM	540						
QY	541	GKLHFLGVSGPVFSFGDPDRVGTAFYQIORGLLEPVALYYPATDALDFRCPRCPVKWHS	600						
Db	541	GKLHFLGVSGPVFSFGDPDRVGTAFYQIORGLLEPVALYYPATDALDFRCPRCPVKWHS	600						
QY	601	GOVPIAKRVFKLRVATIAPLFYTTATLSSVGIALAITFLAFNLHFKLKAIKLSPKLS	660						
Db	601	GOVPIAKRVFKLRVATIAPLFYTTATLSSVGIALAITFLAFNLHFKLKAIKLSPKLS	660						
QY	661	NITAVGCCIFVYATVILLGLDHSFLPSAEDSFATVCTARVYLLSAGFSLAFGSMFAKTYRV	720						
Db	661	NITAVGCCIFVYATVILLGLDHSFLPSAEDSFATVCTARVYLLSAGFSLAFGSMFAKTYRV	720						
QY	721	HRIFRTGSVFKDMLQDITLILVGLLILVDALLVTLVWVTPDPMERHLNLLEISATD	780						
Db	721	HRIFRTGSVFKDMLQDITLILVGLLILVDALLVTLVWVTPDPMERHLNLLEISATD	780						
QY	781	RSVYQPOVEVCRSQTQWLSVLYAYKGLLLVGVYMAWETHRVKIPALNDSQYIGVSU	840						
Db	781	RSVYQPOVEVCRSQTQWLSVLYAYKGLLLVGVYMAWETHRVKIPALNDSQYIGVSU	840						
QY	841	YSVWITSIAVVVLANLISERVTLAFITITATILITSTATICLLFIPKLHDIWARNDIIDP	900						
Db	841	YSVWITSIAVVVLANLISERVTLAFITITATILITSTATICLLFIPKLHDIWARNDIIDP	900						
QY	901	VIHSMGLKMECTRFRVDDRELQYRVQNVYKKEIQALDAEIRKLERLLESGLTTT	960						
Db	901	VIHSMGLKMECTRFRVDDRELQYRVQNVYKKEIQALDAEIRKLERLLESGLTTT	960						
QY	961	STTTSSSLLGGGHLKPELVTSIGISQTPAASKNRTPSISGILNLLLSVLPVPVIPA	1020						
Db	961	STTTSSSLLGGGHLKPELVTSIGISQTPAASKNRTPSISGILNLLLSVLPVPVIPA	1020						
QY	1021	SWPSAEYMQIPMRRSVTFASQPQLEEACLPQADLINRLAHQQAATEAKTLINLRGIFS	1080						

Db	1021	SWPSAEYMQIPMRSVTFASQPLEACLPQADLINRLAHQQAATEAKTLINLRGIFS	1080
QY	1081	RTTSSNGKSTASLADQKGLKAAFKSHMGLFTRLIPSSQTASCNALYNNPNQDSIPSEASS	1140
Db	1081	RTTSSNGKSTASLADQKGLKAAFKSHMGLFTRLIPSSQTASCNALYNNPNQDSIPSEASS	1140
QY	1141	HPNGNHLKPIHRGSLTKSGTHLDHLTKDPNFIPTISGEGDQDTLGGKYVKLLETKVN	1200
Db	1141	HPNGNHLKPIHRGSLTKSGTHLDHLTKDPNFIPTISGEGDQDTLGGKYVKLLETKVN	1200
QY	1201	FQLPSNRRPSVQPPSLRERVGRSPRPHRLPPTCSLSALAESDRPGDSTSLGSK	1260
Db	1201	FQLPSNRRPSVQPPSLRERVGRSPRPHRLPPTCSLSALAESDRPGDSTSLGSK	1260
QY	1261	SIPRISLQQTSGGTWKSMTVGVKSRLSLGDSQEEQQAPANGTE	1305
Db	1261	SIPRISLQQTSGGTWKSMTAGSKRLSLGDSQEEQQAPANGTE	1305
RESULT 3			
Q9BML6 PRELIMINARY; PRT; 1220 AA.			
ID	Q9BML6		
AC	Q9BML6;		
DT	01-JUN-2001 (TReMBLrel. 17, Created)		
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)		
DE	METABOTROPIC GABA-B RECEPTOR SUBTYPE 2.		
GN	GABA-B-R2.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=727;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed-11168554;		
RA	Mezler M., Muller T., Raming K.;		
RT	"Cloning and functional expression of GABA-B receptors from		
RT	Drosophila.";		
RL	Eur. J. Neurosci. 13:477-486(2001).		
DR	EMBL; AF318273; AAK13421.1; -.		
KW	Receptor.		
SQ	SEQUENCE 1220 AA; 137976 MW; 2B33DA2C1A1BDA8B CRC64;		
Query Match 18.3%; Score 1229; DB 5; Length 1220;			
Best Local Similarity 30.5%; Pred. No. 2.2e-82;			
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps 34;			
QY	163	TSRGRPDGLSELGAATWAVEHINRK-RLLPGYTLELVNTQCDPGVGVDRFFHAIYTO	221
Db	48	TGRGVMP-----SVKLAGHVNHEGKILANYRLHWNNDTQCNAAGVKVSKFFDMHSG	100
QY	222	PSTRMVLGSLACSSEVTESLAKVPVNIQVSFGSTSPALSDRREFFPYFYRTVAPDSSH	281
Db	101	PN--KVMLFGAACHTVTDPIAKASKHWHLTQLSYADTHPMFT-KDAFPNFRVVPSENAF	157
QY	282	NPARIAFRKFGWGTVTFTFSQNEEVHSLAVNNLVTELEAANISCAATITPAATDFKQLL	341
Db	158	NAPRLALKFEFNWTRVGTVYQNEPRYSLPHNHVADLDAMEVEVYVETQSF-VNDVAESLK	216
QY	342	LLRETDTRIIGSFQSELAPQILCEAYRLRMFGADYAWILHESMGAPW-PDORTACSNH	400
Db	217	KLREKDVRIILGNFNEHFARFAFCEAYKLDWGRAYQLIMATYSTDMNVTQDSECSVE	276
QY	401	ELQAVENLIVVSTHNSIVGNVSYGLNNHMF---NSQLR-KQSAQFHGQDGFSGVGP	456
Db	277	EIATALEGAAILVDLLPLSTSGDITVAGITADEYLVEYDLRGTYSRFHG-----	326
QY	457	RISIAATQSDSRRRRRGVGTSGGHLFPPEAISQVAPQTYDAVWAIALARAEEHWRN	516
Db	327	-----YTDGIWAAALAIQYVAE-----	344

QY 181 AVEHINKRLLPGYTLLELVNDTCDCPGVGVDRFFHAIYTOPSTRMVMMLLSACSEVTES 240
DB 181 AVEHINKRLLPGYTLLELVNDTCDCPGVGVDRFFHAIYTOPSTRMVMMLLSACSEVTES 240
QY 241 LAKVVPYNNVQVSFGSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIRKFGMGVTTF 300
DB 241 LAKVVPYNNVQVSFGSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIRKFGMGVTTF 300
QY 301 SQNEEVHSLAVNNLVTELEAANTISCAATITFAATDFKEQLLLRETDTRIIGSFQBELA 360
DB 301 SQNEEVHSLAVNNLVTELEAANTISCAATITFAATDFKEQLLLRETDTRIIGSFQBELA 360
QY 361 PQILCEAYRLRMFGADYAVIILHESMGAPWMPDQRTACSNHELQLAVERNLIIVVSTHNSIVG 420
DB 361 PQILCEAYRLRMFGADYAVIILHESMGAPWMPDQRTACSNHELQLAVERNLIIVVSTHNSIVG 420
QY 421 NNVYSGLNNHMFNSQLRKSAQFHGQDGFSGYGPRIISAAATQSDSRRRRRRGVGTSG 480
DB 421 NNVYSGLNNHMFNSQLRKSAQFHGQDGFSGYGPRIISAAATQSDSRRRRRRGVGTSG 480
QY 481 GHLFPEAISQYAPQTYDAVNAIALALRAAEHWRNRNEQSKLDGFDYTRSDMAWEFLQOM 540
DB 481 GHLFPEAISQYAPQTYDAVNAIALALRAAEHWRNRNEQSKLDGFDYTRSDMAWEFLQOM 540
QY 541 GKLEHFGVSGPVFSFGDPDRVCTTAFTYQIORGLLEPVALIYPATDALPRCPRPVKWS 600
DB 541 GKLEHFGVSGPVFSFGDPDRVCTTAFTYQIORGLLEPVALIYPATDALPRCPRPVKWS 600
QY 601 GOVPIAKRVEKLRVATIAFLAFYTIATLSSVGIATLAFNLFHFKLKAIKLSSPKLS 660
DB 601 GOVPIAKRVEKLRVATIAFLAFYTIATLSSVGIATLAFNLFHFKLKAIKLSSPKLS 660
QY 661 NITAVGCIFFYATVILGLDHLSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFAKTVRV 720
DB 661 NITAVGCIFFYATVILGLDHLSTLPSAEDSFATVCTARVYLLSAGFSLAFSGMFAKTVRV 720
QY 721 HRIFTTGSVFKDKMLQDIQIILVGGLLVDALLVILVWVTDPMERHLNLTLEISATD 780
DB 721 HRIFTTGSVFKDKMLQDIQIILVGGLLVDALLVILVWVTDPMERHLNLTLEISATD 780
QY 781 RSVVYQPOVEVCSQHSQHTWLSVLYAYKGLLLVGVYMAWETRVKIPALNDSQYIGSV 840
DB 781 RSVVYQPOVEVCSQHSQHTWLSVLYAYKGLLLVGVYMAWETRVKIPALNDSQYIGSV 840
QY 841 YSVVITSIAIVVLNLANLISERVTLAFITITALTSTTATLCLFLIPKLHDIAWRNDIIDP 900
DB 841 YSVVITSIAIVVLNLANLISERVTLAFITITALTSTTATLCLFLIPKLHDIAWRNDIIDP 900
QY 901 VIHSMGLKMECNTRRFVDDRRRELOYRVEVQNRVYKKEIQALDAEIRKLERLLESGLT 960
DB 901 VIHSMGLKMECNTRRFVDDRRRELOYRVEVQNRVYKKEIQALDAEIRKLERLLESGLT 960
QY 961 STTTSSTSLTGGHGLKPELTVTSGISQTPAASKNTPSTISGLIPNLLLSVLPVPVIPA 1020
DB 961 STTTSSTSLTGGHGLKPELTVTSGISQTPAASKNTPSTISGLIPNLLLSVLPVPVIPA 1020
QY 1021 SWPSAEYMQIPMRSSVTFASQPOLEEAACLPADQLINLRLAHOQAQTEAKTGLINLRGIFS 1080
DB 1021 SWPSAEYMQIPMRSSVTFASQPOLEEAACLPADQLINLRLAHOQAQTEAKTGLINLRGIFS 1080
QY 1081 RTTSSNKGSTASLADQKGLKAAKFSHMGLETRLIPTSPQTSACNAIYNNPNODSIPSEASS 1140
DB 1081 RTTSSNKGSTASLADQKGLKAAKFSHMGLETRLIPTSPQTSACNAIYNNPNODSIPSEASS 1140
QY 1141 HPNGNHLKPIHRSGLTKSGTHLHDKDPNPLIPTITSGGQDQTLGGKVKVKKLETKVN 1200
DB 1141 HPNGNHLKPIHRSGLTKSGTHLHDKDPNPLIPTITSGGQDQTLGGKVKVKKLETKVN 1200
QY 1201 FQLPSNRRPSVWQPPSLRVRGSPRPHRLPPTCSLSALAESDRPQDSTSLGSK 1260
DB 1201 FQLPSNRRPSVWQPPSLRVRGSPRPHRLPPTCSLSALAESDRPQDSTSLGSK 1260
QY 1261 SIPRISLQOVTSGGTWKSMTVGKSRSLSLGDSQEEEOQAPANGTE 1305

DB 1261 SIPRISLQOVTSGGTWKSMTVGKSRSLSLGDSQEEEOQAPANGTE 1305
RESULT 2
Q9VPS7 PRELIMINARY; PRT: 1305 AA.
AC Q9VPS7;
DT 01-MAY-2000 (TREMREL. 13, Created)
DT 01-MAY-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE CG3022 PROTEIN.
GN GABA-B-R3 OR CG3022
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davidson L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003588; AAF51465.2; -.
DR FlyBase; FBgn0031275; GABA-B-R3.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000005; HTHraC.
DR Pfam; PF00003; 7cm3; 1.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:07:33 ; Search time 74.36 Seconds
(without alignments)
2567.044 Million cell updates/sec

Title: US-09-715-962-6
Perfect score: 6705
Sequence: 1 MRIIQVQGTGYPWPAVGL.....RLSLGDSQEEQQAPANGTE 1305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues 473505

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6705	100.0	1305	5 Q9BML5	Q9bml5 drosophila
2	6671	99.5	1305	5 Q9VPS7	Q9vps7 drosophila
3	1229	18.3	1220	5 Q9BML6	Q9bml6 drosophila
4	1228.5	18.3	1221	5 Q9YL33	Q9yl33 drosophila
5	1018.5	15.2	840	5 Q9BML7	Q9bml7 drosophila
6	793.5	11.8	816	5 Q9N502	Q9n502 caenorhabdi
7	530	7.9	1713	5 Q9V3Q9	Q9v3q9 drosophila
8	429.5	6.4	402	5 Q23442	Q23442 caenorhabdi
9	356	5.3	528	5 Q96954	Q96954 geodia cydo
10	350.5	5.2	872	4 Q9H3N6	Q9h3n6 homo sapien
11	336	5.0	983	11 Q62916	Q62916 rattus norv
12	329	4.9	879	11 Q9QY52	Q9qy52 mus musculu
13	311.5	4.6	977	13 Q9PWE1	Q9pwe1 ictalurus p
14	307.5	4.6	976	5 Q9V485	Q9v485 drosophila
15	283.5	4.2	1267	5 Q93564	Q93564 caenorhabdi
16	244.5	3.6	940	13 Q73635	Q73635 fugu rubrip
17	244	3.6	1199	11 Q9EPV6	Q9epv6 mus musculu
18	233.5	3.5	1156	13 Q98UC6	Q98uc6 gallus gall
19	233	3.5	856	13 Q73638	Q73638 fugu rubrip

20	230	3.4	1242	13 Q98UC4	Q98uc4 gallus gall
21	229	3.4	1188	13 Q98UC5	Q98uc5 gallus gall
22	223	3.3	870	5 Q9N4T8	Q9n4t8 caenorhabdi
23	222	3.3	877	13 Q9PW88	Q9pw88 carassius a
24	222	3.3	912	11 Q70410	Q70410 mus musculu
25	218.5	3.3	864	13 Q73637	Q73637 fugu rubrip
26	211.5	3.2	738	5 Q9V4U3	Q9v4u3 drosophila
27	208	3.1	880	13 Q73639	Q73639 fugu rubrip
28	207.5	3.1	848	13 Q93553	Q93553 carassius a
29	206	3.1	253	5 Q23443	Q23443 caenorhabdi
30	204.5	3.0	868	13 Q73636	Q73636 fugu rubrip
31	203	3.0	962	10 Q23048	Q23048 arabidopsis
32	200.5	3.0	153	11 Q9QY85	Q9qy85 rattus norv
33	200.5	3.0	875	13 Q73640	Q73640 fugu rubrip
34	200.5	3.0	941	10 Q9SWD9	Q9swd9 arabidopsis
35	195	2.9	829	10 Q9LFN5	Q9lfn5 arabidopsis
36	194.5	2.9	898	10 Q81776	Q81776 arabidopsis
37	191.5	2.9	551	13 Q9PWQ0	Q9pwq0 fugu rubrip
38	188	2.8	779	11 Q35269	Q35269 rattus norv
39	184	2.7	855	11 Q70409	Q70409 mus musculu
40	180.5	2.7	953	10 Q9ZV67	Q9zv67 arabidopsis
41	179	2.7	877	4 Q9UGT0	Q9ugt0 homo sapien
42	179	2.7	920	10 Q9SHV1	Q9shv1 arabidopsis
43	178.5	2.7	1118	5 Q23496	Q23496 caenorhabdi
44	178	2.7	844	13 Q93552	Q93552 carassius a
45	177.5	2.6	840	11 Q920R8	Q920r8 rattus norv

ALIGNMENTS

RESULT 1

Q9BML5 ID Q9BML5 PRELIMINARY; PRT; 1305 AA.
AC Q9BML5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.
GN GABA-B-R3.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed-11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
Drosophila".
RL Eur. J. Neurosci. 13:477-486(2001).
DR EMBL; AF318274; AAK13422.1; -.
KW Receptor.
SQ SEQUENCE 1305 AA; 143701 MW; 8B8FA80F0E9BEADD CRC64;

Query Match 100.0%; Score 6705; DB 5; Length 1305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRIIQVQGTGYPWPAVGLRLVLALAWATSAAMSAEALQALGHEAIRPGAASISTS 60

Db 1 MRIIQVQGTGYPWPAVGLRLVLALAWATSAAMSAEALQALGHEAIRPGAASISTS 60

QY 61 SPSSPPGESASTVAGTGTPIPPRSDDWKYKRTKVKRRQORLNSHNLPGSTNASHAHLL 120

Db 61 SPSSPPGESASTVAGTGTPIPPRSDDWKYKRTKVKRRQORLNSHNLPGSTNASHAHLL 120

QY 121 NLPPRQRYLVKNQVFESESRMSPAEQMNHGKIVLLGLFELTSGRPRDGLSELGAATM 180

Db 121 NLPPRQRYLVKNQVFESESRMSPAEQMNHGKIVLLGLFELTSGRPRDGLSELGAATM 180

Qy	664	NVFITCLAGAAISLVISDRKDLVFVULSFFII	IFCTTATLCLFVFPKLVELKRNPGVW-D	722
		: : : : : :		
Db	655	nvgimcigaavflrldpnavqfvalvifcstlticlv	fpkltlrlnpdaatqn	714
		: : : : :		
Qy	723	KRYVRATLRPMKNGRSDSSVCELEQ----	RLRDVKNTCRFKALMEKENELQALIRKL-	777
		: : : : : : : :		
Db	715	rrfqtnqkkedskstsvtnqastarleglsenhrl	mtmkiteidkdlceetmqlq	774
		: : : : : : :		
Qy	778	-GPEARKWIDGVCTCGSNVGSELEPILNDDIV	RLSAPPVRRMPSTTVETW- SVDSVVT	835
		: : : : :		
Db	775	dtpekttyfk-----qhnygelndln-----	lgnftestdggkail	811
		: : : : :		
Qy	836	STHIVEMDNSFVSQSTWMAPLPPKKKQSI	VEHHSHAPAPTMWPIQ-QLQCHLQHQH	894
		: : : : : : :		
Db	812	knhlqdn-----pqj-----qwn	tepsrtckdpiedinspehiqrll	849
		: : : : : : :		
Qy	895	QMOQHLLQOQHQQOQOQOQOQHHRHLEK	RNSVSA	931
		: : : : : : :		
Db	850	slqjpl-----hhaylpslggvda	869	
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Search completed: April 30, 2002, 10:00:32
Job time: 575 sec

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Db 595 disirplehcenthmtiwigivaykglmlfgcflawetrnvsipalndskysv 654
QY 664 NVFITCLAGAAISLVSDRKDLVFLVLSFFIIFCTTATLCLVFPKLVKLNPNQGVV-D 722
Db 655 nvgmciigaavsftrdqpvnqfcivalvifstlclvfpkllitrltnpdaatqn 714
QY 723 KRVVATLRPMKNGRRDSSVCELEQ-----RLRDVKNTNCRFKALMEKENELQALIRKL- 777
Db 715 rrfqftqnqkedsktstsvsvngastrelglsenhrmklteldkleevtmqlq 774
QY 778 -GPEARKWIDGVCTGSGVSGSELEPIINDIVRLSAPPVREMPSTTVTEMF-SVDSVT 835
Db 775 dtpekttyik-----qnhyqelndiin-----lgnftestdggkail 811
QY 836 STHVMENSNFVSGVTMAPSLPPKKKQSTVEHSHAPAPTMOPIOQ-OLQOHLQOHO 894
Db 812 knhldqn-----pq-----qwnntpsrtckdpiedinspehiqrrl 849
QY 895 QMOQOHLQOQOHOQOQOQOQOQOQHHRHRLKRNVSVA 931
Db 850 slqipil-----hhaylpsigvda 869

RESULT 15
AA070326
ID AAY70326 standard; Protein: 898 AA.
AC AAY70326;
XX
DT 21-JUN-2000 (first entry)
DE Human gamma amino butyric acid receptor, GABA-B-R2 protein.
KW Gamma amino butyric acid; GABA-B-R2; human; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antiasmatic; antidiabetic;
KW uroathic; analgesic; antitussive; agonist; neuroprotective; nootropic;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 438..461
FT /label= Transmembrane_domain-I
FT Domain 475..501
FT /label= Transmembrane_domain-II
FT Domain 513..535
FT /label= Transmembrane_domain-III
FT Domain 554..576
FT /label= Transmembrane_domain-IV
FT Domain 612..634
FT /label= Transmembrane_domain-V
FT Domain 648..670
FT /label= Transmembrane_domain-VI
FT Domain 676..701
FT /label= Transmembrane_domain-VII
PN W0200012692-AL.
XX
XX 09-MAR-2000.
XX
XX 27-AUG-1999; 99WO-US19651.
XX
XX 27-AUG-1998; 98US-0141760.
XX 16-OCT-1998; 98WO-US22033.
XX 04-NOV-1998; 98US-0186664.
XX 15-DEC-1998; 98US-0211755.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX Jones KA, Laz TM, Borowsky B;
XX
XX
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```
DR WPI: 2000-246751/21.
XX N-PSDB; AA251399.
PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
PT detecting receptor agonists useful for treating e.g. asthma,
PT incontinence, and Alzheimer's disease -
XX
XX Claim 9; Fig 5; 260pp; English.
CC The present amino acid sequence is the human GABA (gamma amino butyric
CC acid)-B-R2 receptor protein isolated from human hippocampus cDNA library.
CC The coding region of GABA-B-R2 is cloned into the expression vector
CC pEX.HRT37 and the plasmid is designated as TL-267 (ATCC No. 203515).
CC GABA-B is a major inhibitory neurotransmitter, the receptors of which
CC are widely distributed throughout the central nervous system. GABA-B-R2
CC receptor has anticonvulsant, antiasmatic, uroathic, analgesic,
CC antitussive, antidiabetic, nootropic and neuroprotective activity.
CC GABA-B-R2 receptor agonists may be used to treat spasticity, asthma,
CC incontinence, drug addiction, Alzheimer's disease, decrease nociception
CC and as an antitussive agent. Transgenic animals with altered GABA-B-R2
CC levels may be used to determine the physiological effects of varying
CC levels of GABA-B-R2 receptor activity.
XX
XX Sequence 898 AA;
SQ
Query Match 24.8%; Score 1590; DB 21; Length 898;
Best Local Similarity 37.5%; Pred. No. 4.3e-121;
Matches 351; Conservative 166; Mismatches 324; Indels 96; Gaps 19;
QY 21 ACQRTAKRSDVYIAGFFPYGDGVENSYTGGRVMPKVKALGALGHVNEHGKILANLYRLHMWN 80
Db 3 scparsatgplsimglmltckevakgsigrgvlpavelaieqrne-sllrpyfldirly 61
QY 81 DTQCNAAVGVKSPFDMHSGPNKVMFLFGAACTHTVTDPIAKSKHWHULTQLSYADTHPMFT 140
Db 62 dtecdnakgikafydaikygnhlmgvfgvcpstvtsiaeslgwnlvqisfaattpvla 121
QY 141 -KDAFFNFRFVPSENAFNAPRLALKEFNWTRVGTVYQNEPRYSLPHNHMVAOLDAMEV 199
Db 122 dkkkpyffrtvpsdnavnpaillkllkhyqkrvgtltqdvqrifsevrnditgvygedi 181
QY 200 EYVETQSFVNDVAESLKKREKDVRIILGNFNEHFAKFAKCEAYKLDWYKQWLMAT 259
Db 182 eisdtessfndpctsvkklgndvriilqfdqmaakvfcceayemgyskywipgw 241
QY 260 YSTDWV---NVTQDSECSVEETATALEGAILVDLLPLSTGDTVAGITADEVLVYDR 315
Db 242 yepswweqvhteanssrclrknlaaamegyigvdfepsskqiktsgktpqqyereynn 301
QY 316 LR-GTEYSRPHGYTDGIWAAALAIQV---AEREDLLTHFDYRVKDWESVFEALR 369
Db 302 krsfgvpskfhgyaydggiwviaktlgrametlhassrhqrlqdfnfdhtlgrilnamn 361
QY 370 NTSFEGVTGVPVRFYNNERKANILINQFQGMERIGBYHSQKSHLDLSLAKPVPKWVGKTP 429
Db 362 etnffgvtgqvfngrmgatiktftqdsrevkvgneynavadtlei-indtirfqsep 420
QY 430 PKDRTLIYIEHSQVNPTIYIVSASVIGVITATVFAFNKIKYRNQYIKMSSPHLNLI 489
Db 421 pkdktiileqlrkisplysilsaltlilmlmasafifnknrnlkikmsspymnli 480
QY 490 IVGCMITLIIIFLGDDTTLSVNAAPFYICTARAWILMAGFSLSFSGAFKSTWVHSIFT 549
Db 481 ilgmisyasiflfgldgsfvsektfetlctvrtwiltvgttafgamfaktwrvhaif 540
QY 550 DLKLNKVKIKDYOLFVMVGVLLAIDIAIITWQIADPFYR--ETKOLEPLHNEID--- 603
Db 541 nvkmkkilkdqkllvvggmllidilicwqavdplrtvteksmep-----dpagr 594
QY 604 DVLVIPENEYCSQSEHMTIFYSIIYAYKGLLLVFGAFLAWETRHYSPALNDSKHGFSVY 663
Db 595 disirplehcenthmtiwigivaykglmlfgcflawetrnvsipalndskysv 654
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Db 496 saflfnknrcklkmsspynmnlilgmslyasayiflfgldgsfvsfektftcltrv 555
 QY 523 AWILMAGSLSFGAMPSKTRWRVHSIFPDLKLNKVKIKDYQLFMVGVGLLAIDIAITWQ 582
 Db 556 twltvgtytafgamfaktwrhaifknvkmkklkdkllvlgvgmllldlcilcwq 615
 QY 583 IADPFYR--ETKOLEPLHLENID----DVLVIPENECQSEHMTIFVSIYAYKGLLLVF 636
 Db 616 avdplrtvkekymep-----dpagrdlsirpllethenthtwlgivaykgllmlf 669
 QY 637 GAFLEWETRVHSIPALNDSKHGFSVYNVFITCLAGAAISLSDRDLVFLVLSFFIF 696
 Db 670 gclawetrvnvsipalndskygmssyvnvgimciigaavsflltrdqpvnqfcivaliif 729
 QY 697 CTTATLCLVFPVKLEKRNQGVV--DKRVTRATLRPMKNGRRDSSVCELEQ-----RLRD 751
 Db 730 cstticlvfpvklitlrtpndaatqnrrfqfqnqkksdstsvtsvnaqstsrlreg 789
 QY 752 VRNTNCRFRKALMEKENELQALIRKL--GPEARKWIDGVVCTGGSNVGSELEPILNDDIV 809
 Db 790 lqsenhrlrmkiteldkleevtmqldqtpkettik-----qnhyqelndlin----- 838
 QY 810 RLSAPPVRRREMPSTTVTEMT--SVDSVTSTHVMENDNSFVSQSTVMAPSLPPKKKKQSIVE 868
 Db 839 -----lgnftestdggkalknhldqn-----pql-----q 864
 QY 869 HHSAPAPTMQPIQO--OLOQHLLQHQHQOQOHLQOQOQOHOQOQOQOQHHRHLEKRN 927
 Db 865 wnttepsrckdpiedinspehigrllslqlpil-----hhaylpsig 907
 QY 928 SVSA 931
 Db 908 gvda 911

RESULT 14

AAY14082
 ID AAY14082 standard; Protein; 898 AA.
 AC AAY14082;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Human GABAR2 protein sequence.
 XX
 KW GABAR2; gamma amino butyric acid class B receptor 2; spasticity; asthma;
 KW incontinence; decreasing nociception; anti-tussive agent; drug addiction;
 KW alzheimer's disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09920751-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 16-OCT-1998; 98WO-US22033.
 XX
 PR 27-AUG-1998; 98US-0141760.
 PR 17-OCT-1997; 97US-0953277.
 XX
 PA (SYNA-) SYNAPTIC PHARM CORP.
 XX
 PI Borowsky B, Jones KA, Laz TM;
 XX
 DR WPI; 1999-302737/25.
 DR N-PSDB; AAX58005.
 XX
 PT Gamma amino butyric acid, class B, receptor 2 polypeptide and gene
 PT sequences
 XX
 PS Claim 9; Fig 2a-d; 260pp; English.
 XX

CC This sequence is the human gamma amino butyric acid, class B,
 CC receptor 2 (GABAR2) polypeptide of the invention. The DNA can be used
 CC for the production of GABAR2, and for the design of probes that are
 CC useful for detection of the DNA or homologues in a sample. Antibodies
 CC against GABAR2 are useful for detecting GABAR2 and GABAR1/R2 on the
 CC surface of cells. Transgenic mice expressing GABAR1/R2 are useful for
 CC determining the physiological effects of varying levels of the receptors
 CC in the presence of an inducible promoter which regulates the receptors
 CC expression. These transgenic mice can also be used to identify GABAR1/R2
 CC antagonists or agonists that are capable of alleviating abnormalities
 CC associated with the receptors. Recombinant cells expressing GABAR1/R2,
 CC or membrane extracts from these cells, are useful for identifying
 CC chemical compounds that specifically bind to the receptor. The cells can
 CC also be used to determine whether the chemical compounds are antagonists,
 CC agonists, activators or inhibitors. Agonists of GABAR1/R2 are useful for
 CC treating spasticity, asthma, incontinence and decreasing nociception. The
 CC agonists can also be used as anti-tussive agents. Agonists are also
 CC useful for treating drug addiction. Antagonists are used to treat
 CC Alzheimer's disease. Functional assays were not possible with GABAR1
 CC alone, so identification of a new GABAR2 polypeptide is useful for high
 CC throughput screening assays for agonists or antagonists against GABAR
 CC receptors using co-expression of GABAR1/R2. The pharmacological and
 CC signal transduction properties of the two receptors GABAR1 and R2 match
 CC those of native GABAR receptors in the brain.
 XX
 SQ Sequence 898 AA;

Query Match 24.8%; Score 1590; DB 20; Length 898;
 Best Local Similarity 37.5%; Pred. No. 4,3e-121;
 Matches 351; Conservative 166; Mismatches 324; Indels 96; Gaps 19;
 QY 21 ACGRTRKSDVIYIAGFFPYGDBGVENSYTGGRVMPGVSKLALGHVNEHGKILANYRLHMMWN 80
 Db 3 scparsatgplisimglmlptkevaksgirgvlpavelaieqrne-sllrpyfidlrly 61
 QY 81 DTQCNAAGVGVKSFDDMHSGPNKVMFLGCACTHTVDTAKASKHWHLQLSYADTHPMFT 140
 Db 62 dtecdnakglkafydaikygnphlmvfgvcpsvtlaeslqgvnlvqlsfaattpvla 121
 QY 141 -KDAFPNFRVVPSENAPRLALLKEFNWTRVTVQNEPRYSLPHNHMVADADAMEV 199
 Db 122 dkkyypfrrtvpnsdnavnpaillkllhyqwrvtcltdqvqrfevnditgvlgedi 181
 QY 200 EVETQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFCEAYKLDYGRAYQWLIMAT 259
 Db 182 eisdtessndpctsvkllkndvrililgqfdqmaakvfccayeenmygskylipgw 241
 QY 260 YSTDWV---NVTQDSECSVEIATALEGAILVDLLPLSTSGDITVAGITADEYLVEDR 315
 Db 242 yepswweqvhteanssrclrknlilaamegyigvdfepisskqiktisgktpqgyereyn 301
 QY 316 LR-GTEYSRFGYTYDGIWAAALAIQYV----AEKREDLLTHFDYRVKDWESVFLEALR 369
 Db 302 krsvgpskfhgaydydgilwaktlqramethasrhqriqdfnfydhtlgrilnam 361
 QY 370 NTSFEGVTGPVRYNNERKANILINQFOLQGMKEITGEYHSKSHDLDSLGRVPKWVGKTP 429
 Db 362 etnffgtvgvfrngermgtikftqfdstevkgyevnavadtlei-indtirfggsep 420
 QY 430 PKDRTLIYIEHSQVNPTIYVSASASVIGVIATVFLAFNFKYRNQRIYKSSPHLNLI 489
 Db 421 pkdtiileqirklslplysiltsaltlilgmasaflfnknrrnqklkkmsspynmnl 480
 QY 490 IVGCMITVLSIIFLGLDPTLSSVAAPFICTARAWILMAGFSLSGFAMFSTWRVHSIFT 549
 Db 481 ilggmlsyasiflfgldgsfvsfektftcltrvltvgttafgamfaktwrhaifk 540
 QY 550 DLKLNKKVKKDYQLFMVGVGLLAIDIAITWQIADPFYR--ETKOLEPLHLENID---- 603
 Db 541 nvkmkklkdkqkllvlgvgmllldlcilcwqavdprrrtvkekymep-----dpagr 594
 QY 604 DVLVIPENECQSEHMTIFVSIYAYKGLLLVFGFLAWETRVHSIPALNDSKHGFSVY 663

QY 289 DLLPLSTSGDITVAGITADEYLVEDRLR-GTEYSRPHGYTYDGIWAALAIQYV----- 342
 Db 318 dfepilsxqktisgktpqgyerennknrgvpskfhgyaydgilwvialktlqramethl 377
 QY 343 AEKREDLLTHFDYRVKDWESVFLALRNTSEGVTPGPRFYNNERKANILINQFOLGOME 402
 Db 378 assrhqriqdfnytdhtlgrilnametnffgtvgvfrngermgtikftqfqsrev 437
 QY 403 KIGEYHSOKSHLDLSLGKPVKWKGTTPKDRTLIYIEHSQVNPITYIVSASASVIGVIA 462
 Db 438 kvgeynavadtlei-indtirfggseppkdtiileqirklisplysilsaltlilmima 496
 QY 463 TVFLAFNIKVRNQRKIKMSSPHLNLIIVGCMITVLSLIFLGLDTLSSVAAPFICTAR 522
 Db 497 saffifnklnrqkiklmsspymnllilgmlsyasiflfgldgsfvsektfetlctvr 556
 QY 523 AWILMAGFSLSFGAMFSTWVRHVSFTDLKLNKKVYKDYQLFMVVGVLALDIAITWQ 582
 Db 557 twiltvgyttafgamfaktwvrhaifnvnmkklkdkqklivvggmllidclilicwq 616
 QY 583 IADPFYR--ETKQLEPLHENID----DVLVIPENEYQCSHMTIFVSIYAYKGLLIVF 636
 Db 617 avdprrtvekysmep-----dpagrdisirpllehcenhtmtiwlglivaykgllmlf 670
 QY 637 GAFLAWETRHSIPALNDSKHIGSVYVNFITCLAGAAISLVSLSRDKDLVFLVLLSFFIIF 696
 Db 671 gcfawetrnvsipalndskyigmsvnyvgimciigaavsfiltrdqpvnqfcivalvliif 730
 QY 697 CTTATLCLVFPKVLKRNQGVV-DKRVRLTRPMSKNGRRDSSVCELEQ----RLRD 751
 Db 731 csttilclvfpkklitlrnpdaatqnrrftqgkqkedsksctsvtsvngqastsrleg 790
 QY 752 VKTNCFRKALMEKENELQALIRKL--GPEARKWIDGVTCTGGSVNGSELEPIILNDIV 809
 Db 791 lqsenhrmrkitedkaleevtmgldtpekttyik-----qnhyeqlndlin---- 839
 QY 810 RLSAPPVRREMPSTVTMT--SVDSVSTHVMEDMSFVSQVSTVMAPSLPPKKKQSIVE 868
 Db 840 -----lgnftestdggkailknhdqn-----pql-----q 865
 QY 869 HHSAPATMMPQIQ-QLQHLQHQHQHQHQHQHQHQHQHQHQHQHQHQHQHQHQHQHQHQ 927
 Db 866 wnttepsrtckdpiedinspenhigrisqlpil-----hhaylpsig 908
 QY 928 SVSA 931
 Db 909 gvda 912
 RESULT 13
 AAY44345
 ID AAY44345 standard; Protein: 965 AA.
 XX
 AC AAY44345;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Protein-2 related to human gb2 GABA B receptor.
 XX
 KW gb2 GABA B receptor; human gb2; Hgb2; calcium-sensing receptor;
 KW gamma-amino butyric acid; 4-amino butanoic acid; GABA;
 KW metabotropic glutamate receptor; neurological disorder;
 KW psychiatric disorder; agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 100
 FT /note= "encoded by GACCTG"
 XX
 FN W09961606-AI.
 XX
 PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11869.
 XX 29-MAY-1998; 98US-0087274.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Clark J, Bonner TI;
 XX WPI; 2000-105616/09.
 DR N-PSDB; AA229447.
 XX New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor,
 PT useful for identification of (ant)agonists and for treatment of
 PT neurological disorders
 XX Disclosure; Page 60-62; 67pp; English.
 CC The present sequence is a protein related to human gb2 GABA B receptor.
 CC Human gb2 (Hgb2) shares sequence homology with rat GABA B receptor rgbl,
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate
 CC receptors. It can be produced in host cells by transforming them with
 CC recombinant expression vector comprising hgb2 encoding cDNA. The cells
 CC that express the receptor are used in the development of drugs for
 CC treatment of neurological and psychiatric disorders, for pharmacological,
 CC physiological, functional, or other investigational analysis of gb2
 CC GABA B receptor, its agonists or antagonists and for determining the
 CC ability of a chemical to bind to a mammalian gb2 GABA B receptor in
 CC vitro. They may also be used for the preparation of antibodies to hgb2
 CC which can be used in diagnostic assays.
 CC Note: There is no relevant information given about this sequence in the
 CC specification.
 XX Sequence 965 AA;
 SQ
 Query Match 24.8%; Score 1591.5; DB 21; Length 965;
 Best Local Similarity 37.3%; Pred..No. 3.6e-121;
 Matches 360; Conservative 165; Mismatches 328; Indels 111; Gaps 22;
 QY 8 PFASLLFLLL-----WSTACGRATKRS-DVYIAGFPYGDGVNSTGTGRVM 53
 Db 19 pparllllllllllplagawgargaprrpppsplsimgImpltkevagsigrvl 78
 QY 54 PSVKLAGLVHNEHGKILANRLHMWNDTCNAAVGVKSFDDMMHSPKNKVMIFSGAACTH 113
 Db 79 pavelaieqirne-silrpyfldrly-dtecdnakgikafydaikygnphlmvfggvcp 136
 QY 114 VTDPiAKAKSHWHLTQLSYADTHPMFT-KDAFPNFRFPVPSNAFAPRALLLKEFNWTR 172
 Db 137 vtsiaeslggnlvqlsfaattpvladkkkypffftvpsdnavnopailkllkhyqwr 196
 QY 173 VGTVYQNEPRYSLPHNHMADLDAMEVEVETQSFVNDVAESLKKREKDVRIILGNFNE 232
 Db 197 vgtltqdvqrfservndltglvgedieidsfdesfndpctsvkklkgndvriilgqfdq 256
 QY 233 HFARKAFCEAYKLDVGRAYOWLIMATYSTDW---NVTQDSCESEETATALEGAILV 288
 Db 257 nmaakfvccaeenmygskvqwiipgwyepsweweqvteanssrlrknllaamegyiv 316
 QY 289 DLLPLSTSGDITVAGITADEYLVEDRLR-GTEYSRPHGYTYDGIWAALAIQYV----- 342
 Db 317 dfepilsxqktisgktpqgyerennknrgvpskfhgyaydgilwvialktlqramethl 376
 QY 343 AEKREDLLTHFDYRVKDWESVFLALRNTSEGVTPGPRFYNNERKANILINQFOLGOME 402
 Db 377 assrhqriqdfnytdhtlgrilnametnffgtvgvfrngermgtikftqfqsrev 436
 QY 403 KIGEYHSOKSHLDLSLGKPVKWKGTTPKDRTLIYIEHSQVNPITYIVSASASVIGVIA 462
 Db 437 kvgeynavadtlei-indtirfggseppkdtiileqirklisplysilsaltlilmima 495
 QY 463 TVFLAFNIKVRNQRKIKMSSPHLNLIIVGCMITVLSLIFLGLDTLSSVAAPFICTAR 522


```
XX Sequence 941 AA;
SQ
Query Match 24.9%; Score 1598; DB 22; Length 941;
Best Local Similarity 37.3%; Pred. No. le-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;
QY 8 PFASLFLLL-----WSTACGRFAKRS-DVYIAGFFPYGDGVNSYTGKGV 53
D 11 11 11
D 19 pparlllllllllplapagawgargapppssplimglmltkevagsigrv 78
D 11 11 11
QY 54 PSVKLALGHVNEGKILANRYLHWNNDTOCAAVGVKSPFDMHSGPNKVMFLFGA 113
D 11 11 11
D 79 pavelaieqrne-sllrpyflrdlrydtecdnagkafaydaikygnhlmvggvcps 137
D 11 11 11
QY 114 VTDPIAKASKHHLTOLSYADTHPMFT-KDAFPNFRFPVSENAFAPRLALLKEFNW 172
D 11 11 11
D 138 vtsiaeslgwnlvlsfaattpvldkkyfpyftrvpsdnavnpaillklkhyqwr 197
D 11 11 11
QY 173 VGTVQNEPRYSLPHNHMADLDAMEVEVYVETQSFVNDVAESLKKREKDVRIILGN 232
D 11 11 11
D 198 vgtltdqvrfservndltvlygedieidsfndpctsvkklgndvriilgfdq 257
D 11 11 11
QY 233 HFARKAFCEAYKLDYKGRAYQWILMATYSTDW-----NVTQDSECSVEETA 288
D 11 11 11
D 258 nmaakvfcaeyeenmygskqwlipgwypswweqvhteansrcrlknlamegyiv 317
D 11 11 11
QY 289 DLLPLSTSGDITVAGITADEYLVYEDRLR-GTEYSRPHGYTYDGIWAAALAIQV 342
D 11 11 11
D 318 dfeplskqiktisgtpqyereynknrgsvpskfhgyaydgviwaktlqrametlh 377
D 11 11 11
QY 343 AEKRELLTHFYRVKDWESVFLALRNTSFEQVPRFYNNERKANILINQFQLQME 402
D 11 11 11
D 378 asrhqridqfnytdhtlgrilnamnetnfgvtgqvfrngermgtikftqgdsrev 437
D 11 11 11
QY 403 KICEYSQSKHLDLSLGGPKVKWGVKPPKDPRTLIYIHSQVNPITYIVSASVIGV 462
D 11 11 11
D 438 kvgeynavadtlei-indtirfgseppkdktilleqlrkisiplylsalttilgm 496
D 11 11 11
QY 463 TVFLAFNIKNRYIKMSPNLIIVGCMITYLSIIFGLDITLSSVAAPFYICTAR 522
D 11 11 11
D 497 safllfnknrdgkllkmsppymnliilgmsisayeflfgldgsfvsektfclctvr 556
D 11 11 11
QY 523 AWILMAGFSLSGAMPKTRVHSIFDLKLNKVKIKDYQLFMVGVLLAIDIAITWTQ 582
D 11 11 11
D 557 twiltvgyttafagmfaktwrhvfhaifknvkmkkkikdkqllvivggmllidclicwq 616
D 11 11 11
QY 583 IADPFYR--ETKQLEPLHENDID----DVLVIPENECQSEHMTIFVSIYAYKGLLV 636
D 11 11 11
D 617 avdplrtvtekysemep-----dpagrdisrpllehcenhtmtiwigvyaykglmlf 670
D 11 11 11
QY 637 GAFLWETRHVSIPALNDSKHGFSVYNVFTITCLAGAAISLVLSDRKDLVFLLSFF 696
D 11 11 11
D 671 gclawetrvnsipalndskysgynvngimclgaavsflltrdpnvqfcivalvif 730
D 11 11 11
QY 697 CTTATCLVFPVKLVKLPQGVW-DKVRATLRPMKNGRRDSSVCELEQ-----RLRD 751
D 11 11 11
D 731 csticllvfpvklitrltnpdaatqnrrfftgnqkkskdststsvtnqastslreg 790
D 11 11 11
QY 752 VNTNCRFRKALMEKENELQALRKIL--GPEARKWIDGVVCTGGSNVGSLEPLTND 809
D 11 11 11
D 791 lqsenhrlmkitelkdleevtmqldtpekttyik-----qnhyqelndiln--- 839
D 11 11 11
QY 810 RLSAPPVRREMTSTVTEMT-SVDSVTSTHVMENDSFVSQSVTMAPSLPPKKKKQSI 868
D 11 11 11
D 840 -----lgnftestdggskalknhldqn-----pql-----q 865
D 11 11 11
QY 869 HHSHAPAPTMOPIQO-QLQOHLQHQOQOQOHLQOQOQOQOQOQOQOQOQHHRHLE 927
D 11 11 11
D 866 wnttepsrtckdpiedinspehigrslrlqlpil-----hhaylpsig 908
D 11 11 11
QY 928 SVSA 931
```

D 909 gvda 912

RESULT 10
AA568743
ID AAY68743 standard; Protein; 941 AA.

XX AAY68743;

XX 05-MAY-2000 (first entry)

XX A human gamma-amino-butyric acid-B2 receptor.

XX Human; gamma-amino-butyric acid receptor; GABA receptor; GABA-B2;
KW G-protein coupled receptor; neurotransmitter; chromosome 9;
region 9q21.

XX Homo sapiens.

XX Key Location/Qualifiers

FH Domain 1..480

FT /note= "extracellular domain"

FT Domain 481..494

FT /note= "hydrophobic domain"

FT Domain 518..545

FT /note= "hydrophobic domain"

FT Domain 558..578

FT /note= "hydrophobic domain"

FT Domain 597..618

FT /note= "hydrophobic domain"

FT Domain 653..676

FT /note= "hydrophobic domain"

FT Domain 691..713

FT /note= "hydrophobic domain"

FT Domain 719..743

FT /note= "hydrophobic domain"

XX WO20000602-A1.

XX 06-JAN-2000.

XX 29-JUN-1999; 99WO-AU00524.

XX 29-JUN-1998; 98AU-0004384.

XX (GARV-) GARVAN INST MEDICAL RES.

XX Herzog H;

XX WPI; 2000-170911/15.

XX N-PSDB; AAZ46129.

XX New nucleic acid used to produce recombinant protein for screening for
specific agonists and antagonists, potential therapeutics -
Claim 3; Fig 1; 27pp; English.
The present sequence represents a human gamma-amino-butyric acid
(GABA)-B receptor, designated GABA-B2. The protein is a transmembrane
G-protein coupled receptor which is activated by the neurotransmitter
GABA. Brain tissue has the highest expression of human GABA-B2 mRNA,
especially in the cerebellum, cerebral cortex, occipital pole, frontal
lobe, and temporal lobe. The GABA-B2 gene is located on chromosome 9,
in the region 9q21. Antagonists and agonists of the GABA-B2 protein
are potential therapeutic agents. A GABA-B2 polynucleotide that is a
dominant negative mutant can be used to reduce or eliminate expression
of endogenous GABA-B2 protein, while antisense sequences and ribozymes
are used to prevent translation of GABA-B2.

XX Sequence 941 AA;

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Clark J, Bonner TI;
 XX WPI: 2000-105616/09.
 DR N-PSDB; AAZ29422.
 XX New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor,
 PT useful for identification of (ant)agonists and for treatment of
 PT neurological disorders
 XX Claim 9; Page 26-28; 67pp; English.
 XX The present sequence is human gb2 GABA B receptor subunit. Human gb2
 CC (Hgb2) shares sequence homology with rat GABA B receptor rgbl,
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate
 CC receptors. It can be produced in host cells by transforming them with
 CC recombinant expression vector comprising hgb2 encoding cDNA. The cells
 CC that express the receptor are used in the development of drugs for
 CC treatment of neurological and psychiatric disorders, for pharmacological,
 CC physiological, functional, or other investigational analysis of
 CC gb2 GABA B receptor, its agonists or antagonists and for determining the
 CC ability of a chemical to bind to a mammalian gb2 GABA B receptor in
 CC vitro. They may also be used for the preparation of antibodies to hgb2
 CC which can be used in diagnostic assays.
 XX
 SQ Sequence 941 AA;

Query Match 24.98; Score 1598; DB 21; Length 941;
 Best Local Similarity 37.3%; Pred. No. 1e-121;
 Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;
 QY 8 PFASLLFLL-----NSTACGRTRAKRS-DYIAGFFPYGDCVENSYTCRGVM 53
 DB 19 pparlllllllpllapgawgargarpppsppslimglptkevaksigrvli 78
 QY 54 PSVKLALGHVNEHGKILANYRLHWMNDTCNAAGVKSFFDMHSGPNKVMFLGAACTH 113
 DB 79 pavelaieqrne-sllrpyfldrltydtecdnaglkafydaikygnphlmvfgvcps 137
 QY 114 VTDPITAKSKHHHTQLSYADTHPMFT-KDAPPNFRVVPSPNAPNRLALLKEFNWTR 172
 DB 138 vtsilaeslgwnlvqlsaftatpvladkkykpyfrtvpnsnavnpaillkilkhyqwr 197
 QY 173 VGTYYQNEPRYSLPHNHVADLDAVEVEVETQSPVNDVAESLKKLREKDVRIILGNFNE 232
 DB 198 vgtltgqvrfsevrndltgylgedleisdesfsndpctsvkklkgndvriilgqfdq 257
 QY 233 HFARKAFCEAYKLDWYGRAYOWLIMATYSTDW-----NVTDSECSVEEITALEGAILV 288
 DB 258 nmaakvfccayeemngskyqwiipgwyepswewqvhteanssrclrknl laamegyigv 317
 QY 289 DLLPLSTSGDITVAGITADEYLVEYDLRL-GTEYSRFGHYTDYGIWAALAIQYV----- 342
 DB 318 dfeplsskqiktisgktpqpyereynnrsgvpskfbyaydgiwviaktlqrametlh 377
 QY 343 AEKREDLLTHFDYRVKDWESVLEALRMTSECVTPGVFRFYNNERKANILINQFOLGQME 402
 DB 378 assrhqrlqdfnytdhtlgrillnamnetnfgvtgqvfrngermtgikftqfqsrev 437
 QY 403 KIGYHSGKSHLDLSLGRPVKVGWTPPKDRTLIVIEHSONVNTPIVVSASASVIGVITA 462
 DB 438 kvgeynavadtlei-indtirfgseppkktilleqrlkislpiylsalsaltlglmma 496
 QY 463 TVFLAFNIKRYNORYIKMSSPHNLNLIIVGCMITLSIFLGLDRTLSSVAAPFVICTAR 522
 DB 497 safifnknrnqkllkmsppymnlilgmlsyasiflglsgsfvsektfetlctr 556
 QY 523 AWILMAFSLSFGAMFSTWRVHSTFTDLKLNKKYKIDQVQLPMVGVLLAIDAITTWO 582
 DB 557 twilitvyttafmgafaktwrvaifknvkmkklkldqklivivgmlldicilicwq 616

QY 583 IADPFYR--ETKOLEPLHHEID-----DVLVIPENEYCOSEHMTIFVSIYAYKGLLVF 636
 DB 617 avqplrttvekysmep-----dpagrdisrpllehcenhtmtwiigivaykglmlf 670
 QY 637 GAF LAWETRVSTPALNDSKHIGFSYVNVFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
 DB 671 gcf lawetrvnsipalndskysigmsvynvglmciigaavsfltrdqpnvqfcivalvlf 730
 QY 697 CTTATLCLVFPVKLVKRNPOGVV-DKRVRAVLRLPMKNGRRDSSVCELEQ-----RLRD 751
 DB 731 cstittclvfpvklitrtlpdaatqrrfqtgnqkksktsvtsvngqastrlieg 790
 QY 752 VKNTRCFRKALMEKENELQALIRKL--GPEARKWIDGVTCGSGNSVGESEILNDIV 809
 DB 791 lqsenhrllrmkitedkdeevlmgldtpekttyik-----qnhyqelindiln---- 839
 QY 810 RLSAPPVRREMPSTVTYEMT-SVDSVTSTHVEDMNSFVSOSTVMAPSLPPKKKQSIIVE 868
 DB 840 -----lgnftestdggkailknhldgn-----pqj-----q 865
 QY 869 HHSAPAPTMMPQITQO-QLOOHLQOHOOMOOOHLQOOHOOMOOOQOOHHHRLKRN 927
 DB 866 wntcepsrtckdpiedinspehigrllslqplil-----hhaylpsig 908
 QY 928 SVSA 931
 DB 909 gvda 912
 RESULT 9
 AAB50088
 ID AAB50088 standard; Protein; 941 AA.
 XX AAB50088;
 AC AAB50088;
 XX 19-MAR-2001 (first entry)
 XX HG20 protein sequence.
 XX Human; HG20; gamma-amino-butyric acid receptor; GABA-B.
 XX Homo sapiens.
 OS Wo2000073788-AL.
 PN 07-DEC-2000.
 PD 30-MAY-2000; 2000WO-CA00638.
 PF 01-JUN-1999; 99US-0137025.
 PR (MERI) MERCK FROSST CANADA & CO.
 XX Ng G, O'Neil G;
 PI WPI: 2001-049959/06.
 XX N-PSDB; AAC91906.
 XX Use of gabapentin, l-(aminomethyl)cyclohexanecarboxylic acid, in assays for
 PT identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists
 PT
 PS Claim 2; Fig 3; 85pp; English.
 XX The present invention relates to a method for determining whether a
 CC substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a
 CC potential agonist or antagonist of the GABA-B receptor. The method
 CC comprises exposing cells to l-(aminomethyl)cyclohexanecarboxylic acid
 CC (gabapentin) in the presence or absence of the substance under
 CC investigation. The present sequence is human HG20, which was used in the
 CC present invention to construct a functional GABA-B receptor, for use in
 CC the method of the present invention.

CC GABAB-R2 as well as a novel, functional GABAB receptor comprising
CC a heterodimer of GABAB-R1 and GABAB-R2 receptor subunits. It also
CC relates to variants of the receptors, nucleotide sequences encoding
CC the receptors, vectors, stable cell lines, antibodies, screening
CC methods, methods of receptor production, and methods of treatment
CC or prophylaxis of a disorder that is responsive to modulation of
CC GABAB receptor activity using a compound that has GABAB receptor
CC modulating activity. The disorder is especially a CNS disorder, a
CC gastrointestinal disorder, a lung disorder or a bladder
CC disorder, especially spasticity, epilepsy, Alzheimer's disease,
CC pain or an affective or feeding disorder (claimed).
XX
SQ Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 21; Length 941;
Best Local Similarity 37.3%; Pred. No. le-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLLFLLL-----WSTACGRTAKRS-DVYIAGFFPYGDGVNSYTGGRVGM 53
Db 19 pparllllllllppllapagwargprpppsppslimglmltkevaksigrv1 78
QY 54 PSVKLALGHVNEHGKILANRLHMMWNDTCNAAVGVKSFDDMMHSGPNKVMFLFGAACTH 113
Db 79 pavelaieqirne-silrpyfldrlydtecdnakgkafydaikygnphlmvfgvcps 137
QY 114 VTDPIAKAKSHWHLTQLSYADTHPMFT-KDAFPNFRVPSPSENAFNAPRLALLKEFNWTR 172
Db 138 vtsiaeslqgnlvqlsaftcpvldadkkypffrtvpsdhavnpailklkhyqwr 197
QY 173 VGTIVYQNEPRYSPLPHNMVADLDAVEVEVETQSFVNDVAESLKLREKDVRIILGNFNE 232
Db 198 vtltdqdvrfsevrndltgvlgedieidsfndspctsvkklgndvrililgfdq 257
QY 233 HFARKAFCEAYKLDYGRAYOWIMATYSTDWN---NVTQDSECSVEETATALEGAILV 288
Db 258 nnaakvfccayeenmgygkyqlipwypeswqevhteansrcrlrknllaamegyiv 317
QY 289 DLLPLSTSGDITVAGITADELYVEYDLRLR-GTEYSRPHGYTYDGIWAAALAIQV----- 342
Db 318 dfeplsskqiktisgtpqgyereynkrsgvgsfkfhgyaydgviaktlgrametlh 377
QY 343 AKREDLLPHFDYRVKDWESVFLEARNFSGVTGVPVRYNNERKANILINQFQLQOME 402
Db 378 assrhqridqfnydhtlgrilinnamnetnfgvtgqvvrngermgtikftqfqsrev 437
QY 403 KIGEVHSQKSHLDLSLGGPKVKKVTPPKDRTLIYIEHSQVNPITYIVSASVIGVILIA 462
Db 438 kygeynavadtiei-indtirfgsppdkdtillqlrksisplylsalsaltlilgmima 496
QY 463 TVFLAFNIKRYNQRYIKMSPLNNLIIVGCMITYLSIIFLGLDTLSSVAAPFYICTAR 522
Db 497 saflfnknknqkklkmsppmnnliilggmlsyasiflfigdgsfvsektfctlctr 556
QY 523 AMILMAGFSLSGAMESKTRVRSIHSTDLKLNKVTINDVQLFMVGVLLAIDAITWQ 582
Db 557 twlltvgtytafgamfaktwrhaifknvkmkkkikdkllvlgvgmllidicilicwq 616
QY 583 IADPFVR---ETKQLEPLHENDID---DVLVIPENECYCOSEHMTIFVSIIVAYKGLLVF 636
Db 617 avdplrlrtvekysmep-----dpagrdlsirpillecenthmtlwiglvaykgmlmlf 670
QY 637 GAFLAWETHRVSTIPALNDSKHIGFSVYNYFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
Db 671 gcflawetrvnsipalndskylgmsvynvgimciigaavsfllrtdqnpvqfivalvif 730
QY 697 CTTATLCLVFPKLVKRNQGVG-DKRVRAFTRPMSKNGNRDSSVCELEQ-----RLRD 751
Db 731 cstiticlvfpklltrtpdaatqnrffqtnqkdkedsktsvtsvtnqastslreg 790
QY 752 VKNTRCFKALMEKENELQALIRKL--GPEARKWTDIGVCTCGSNVGSLEPILNDDIV 809

Db 791 lqsenhrirmkiteldkdleevtmqlqdtpekttylk-----qnhyqelnidln---- 839
QY 810 RLSAPPVRRPSTVTEMT-SVDSVTSTHVEDMNSFVSQVTVMAPSLPPKKKKQSIVE 868
Db 840 -----lgnftestdgkailknhldqn-----pgl-----q 865
QY 869 HSHAPATMMQPIQQ-QLQQHLQQHQMOQOHLQQOQHQMOQOQOQOHHHRHLEKRN 927
Db 866 wnttpestrctkdpliedinspehigrslslqplil-----hhaylpsig 908
QY 928 SVSA 931
Db 909 gvda 912
RESULT 8
AAY44342
ID AAY44342 standard; Protein; 941 AA.
XX AAY44342;
XX
DT 14-MAR-2000 (first entry)
XX Human gb2 GABA B receptor.
XX gb2 GABA B receptor; human gb2; Hgb2; calcium-sensing receptor;
KW gamma-amino butyric acid; 4-amino butanoic acid; GABA;
KW metabotropic glutamate receptor; neurological disorder;
KW psychiatric disorder; agonist; antagonist.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 90
FT Modified-site 298 /note= "Potential N-linked Glycosylation site"
FT Modified-site 404 /note= "Potential N-linked Glycosylation site"
FT Modified-site 453 /note= "Potential N-linked Glycosylation site"
FT Domain 1..476 /note= "Potential N-linked Glycosylation site"
FT /label= Amino-terminal_region
FT /note= "Extracellular"
FT Domain 477..503
FT /label= Transmembrane_domain_1
FT /note= "Hydrophobic and Putative"
FT Domain 519..543
FT /label= Transmembrane_domain_2
FT /note= "Hydrophobic and Putative"
FT Domain 551..573
FT /label= Transmembrane_domain_3
FT /note= "Hydrophobic and Putative"
FT Domain 594..617
FT /label= Transmembrane_domain_4
FT /note= "Hydrophobic and Putative"
FT Domain 654..675
FT /label= Transmembrane_domain_5
FT /note= "Hydrophobic and Putative"
FT Domain 692..712
FT /label= Transmembrane_domain_6
FT /note= "Hydrophobic and Putative"
FT Domain 718..746
FT /label= Transmembrane_domain_7
FT /note= "Hydrophobic and Putative"
XX WO9961606-A1.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11869.
XX 29-MAY-1998; 98US-0087274.
PR

QY 54 PSLKALGHVNEHGKILANYRLHMMWNDCQNAAGVSKSFDDMHSGPNKVMFLGAACTH 113
Db 79 pavelaieqrne-silrpyfldrllytecdnagklafydaikygnphlmvfgvcpes 137
QY 114 VTDPIDAKSKHHLTQLSYADTHPMFT-KDAFPNPFRRVVPVPSNAPNAPRLALLKFEFNWTR 172
Db 138 vtsiaeslqgnlvqlsfaattvpvlaadkkypyffrtvpsdnavnvpailkllkhyqwr 197
QY 173 VGTYYQNEPRYSLPHNHMVAOLDMAEVEVEVETQSVNDVAESLKKLRKDKDVRILGDNFE 232
Db 198 vgtltqdvrfsevrndltgylgediesdtesfndpctsvkklkgnndvrlilgqfdq 257
QY 233 HFARKACEAYKLDWYGRAYOWLIMATYSTDW-NTQDSECSVEEIALALEGAILV 288
Db 258 nmaakvccayeeenmygkyqwilpgwepswqevhteanssrcrlrknllaamegyigv 317
QY 289 DLLPLSTSGDITVAGITADEYLVEYDLR-GTEYSRFGHYTYDGIWAALAIQYV---- 342
Db 318 dfepsskqiktisgktpqgyereynkrsgvgpskfgyaydglwviaktigrametlh 377
QY 343 AEKREDLLTHEDYRVKDWESVLEALRNTSFEGVTGPVRYNNERKANILINQFOLGQME 402
Db 378 assrhqrdqfnytdhtlgrilnamnetnffvgvqvvfrngermgtkikftqfdqstev 437
QY 403 KIGEYHSQKSHLDLSLGRPVKVGKTPPKDRTLVIHESQVNPITYVSASASVIGVITA 462
Db 438 kvgeynavadtlei-indtirfgsepkktilleqirkiislpysalisaltlilgmlma 496
QY 463 TVFLAFNKKYRNQRYIKMSSPHNLNLTIVGCMITVLSIFLGLDITLSSVAAPFVICTAR 522
Db 497 safflfnknknqkllmsspymnllilgmsyaslflgldgsvfsektfetictvr 556
QY 523 AWILMAGFSLSFGAMFSTWRVHSITFDLKLKVKIKDYQLPMVVGVLIAIDIAITTTWQ 582
Db 557 twiltvgytafagmfaktwrvaifknvkmkikiqkllivvggmllidclilicwq 616
QY 583 IADPFYR--ETKQLEPLHENDID----DVLVTPENEXCOSEHMTIFVSTIYAYKGLLVF 636
Db 617 avdplrtvkekysmep-----dpagrdisirpllehcenhtmtlwlgiyaykylmlif 670
QY 637 GAFLAWETRHVSIPALNDSKHGFSVYVNVFTCLAGAAISLVLSDRKLDFVLLSFFIIF 696
Db 671 gcfawetrvnsipalndskylgmsvnyvglmciigaavsfiltrdqpvnqfcivalviif 730
QY 697 CTTATLCIVFPKLVKELRQGVV-DKRRVATLRPMKNGRRDSSVCELEQ-----RLRD 751
Db 731 cstlilelvfpkilitrnpdaatqnrrftqtkkedststsvtsvngqastsrleg 790
QY 752 VKNTNCRPKALMEKENELQALIRKL--GPEARKWIDVTCGTGGSNVGSELEPILNDDIV 809
Db 791 lqsenhrmrkkiteldkdeevtmqlqdtpekttyik-----qnhyqelndiin---- 839
QY 810 RLSAPPVRRRNPSTVTEMT-SVDSVSTHVEDMSFVSQSVTVNAPSILPPKKKQSIVE 868
Db 840 -----lgnftestdggkailknhldqn-----pql-----q 865
QY 869 HHSAPATMMQPIQQ-OLQOHLQOHOQOQOHLQOQOHOQOQOQOQOHHHRHLEKRN 927
Db 866 wntteprtckpiedinspehqrirlslqilpil-----hhaylpsig 908
QY 928 SVSA 931
Db 909 gvda 912

RESULT 7
ID AAY79202
AC AAY79202 standard; Protein; 941 AA.
XX AAY79202;
XX AAY79202;
DT 19-JUN-2000 (first entry)
XX

DE Human GABAB receptor 2.
XX
KW GABAB receptor 2; GABAB-R2; human; bladder disorder;
KW gastrointestinal disorder; central nervous system disorder;
KW lung disorder; spasticity; epilepsy; Alzheimer's disease; pain;
KW affective disorder; feeding disorder; diagnosis; therapy;
KW G-protein coupled receptor; GABA; gamma-aminobutyric acid;
KW signal transduction.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..41
FT Protein /note= "signal peptide" 42..941
FT Domain /note= "mature protein" 481..504
FT Domain /note= "transmembrane domain I" 519..544
FT Domain /note= "transmembrane domain II" 557..578
FT Domain /note= "transmembrane domain III" 597..618
FT Domain /note= "transmembrane domain IV" 654..676
FT Domain /note= "transmembrane domain V" 690..713
FT Domain /note= "transmembrane domain VI" 719..744
FT Domain /note= "transmembrane domain VII" 90
FT Modified-site /note= "N-glycosylated" 298
FT Modified-site /note= "N-glycosylated" 389
FT Modified-site /note= "N-glycosylated" 404
FT Modified-site /note= "N-glycosylated" 453
FT Modified-site /note= "N-glycosylated"
XX WO200014222-A2.
PN 16-MAR-2000.
PD
XX 03-SEP-1999; 99WO-GB02918.
XX
PR 07-SEP-1998; 98GB-0019420.
PR 09-OCT-1998; 98US-0103670.
XX (GLAX) GLAXO GROUP LTD.
XX Barnes AA, Wise A, Marshall FH, Fraser NJ, White JHM, Foord SM;
XX WPI; 2000-256974/22.
XX N-PSDB; AA294168.
XX
XX GABA-B receptor subtypes useful for identifying modulators of GABA-B
XX receptor activity that may be used for preventing and treating diseases
XX including Alzheimer's disease, epilepsy and spasticity -
XX Claim 11; Fig 1B; 67pp; English.
XX
XX The present sequence is that of a novel human GABAB receptor
XX subtype, GABAB-R2, as deduced from a cDNA clone (see AA294168)
XX isolated from human cerebellum cDNA on the basis of homology to
XX rat GABA-R1a and 1b splice variants. GABAB receptors are members
XX of the 7-transmembrane G-protein coupled receptor superfamily
XX Activation results in signal transduction through a variety of
XX pathways mediated principally via members of the Gi/Go family of
XX pertussis toxin-sensitive G-proteins. GABAB-R2 is specifically
XX expressed at high levels only in the central nervous system (CNS).
XX The invention relates to novel GABAB subtypes GABAB-RLC and

CC of (A) with G-proteins or other signal transduction molecules. The
CC analysis of the interactions of (A) and GABA-B receptors is important
CC for identifying potential active substances against diseases such as
CC epilepsy, stroke and psychological diseases such as stress, manic
CC depression, schizophrenia, migraine and others. This sequence represents
CC the human GABA-B receptor described in the invention.
XX
SQ Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 21; Length 941;
Best Local Similarity 37.3%; Pred. No. 1e-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLFLLL-----WSTACGRATKRS-DVVIAGFFPYGCGVENSYTGGRVM 53
DB 19 pparlllllllllplapagwargapppspisimglpltkvaksgirgvl 78
QY 54 PSVKLALGHVNEHGKILANYRLHWMNDTQCNAAGVGSFFDMHSGPNKVMFLFGAACH 113
DB 79 pavelaieqrne-sllrpyfldrllydtecdnaklkafydaikygnhlmvfgvcps 137
QY 114 VTDPIDAKASHWHLTOLSYADTHPMFT-KDAFPNFRVVPSENAPNAPLALLKKEFNWTR 172
DB 138 vtsiaeslqgmnlvqlsfaattppvadkkyfpyfrtvpnsnavnpaillkilkhyqwr 197
QY 173 VGTQYQNEPRYSLPHNHMADLAMEVSEVETQSFVNDVAESLKKLRKDVRIILGNFNE 232
DB 198 vgtitqdvrfsevrndltgylgedieisdtcesfndpctsvkklkndvriilgqfdd 257
QY 233 HFARAFCEAYKLDYGRAYQWIMATYSTDMW-----NVTQSECSVEIATALEGAILV 288
DB 258 nmaakvfccayeenmygkyqwiipgwypeswqevhteansrrclrknlleaamegyigv 317
QY 289 DLLPLSTSGDITVAGITADEYLVEYDRLR-GTEYSRFHGYTYDGIWAALAIQYV----- 342
DB 318 dfeplsskqlktisgktqpyereynnrsgvgsfkfgyaydgiwviaktlgrametlh 377
QY 343 AEKREDLLTHFDYRVKDWESFLEALNRTSFGVGPVRYNNERKANILINQFOLGOME 402
DB 378 assrhqriqdfnytdhtlgrilnamnetnffgvtgvvfrngerngtikftqfddsrev 437
QY 403 KIGYHQSOKSLDLSLGRPKWVGKTPPKPRDLIYIEHSQVNPTIYIVSASAVIGIITA 462
DB 438 kvgeynavadtlet-indtirfgseppkdktilleqirklisplysilsaltlilgmlma 496
QY 463 TVFLAFNIKRYNORYIKMSSPHLNLIIVGCMITLISLIIFGLDITLSSVAAPPYICTAR 522
DB 497 safifniknrnqkllkmspsymnnlilgmlsyasiflglgdfsvsektfctetlctvr 556
QY 523 AWILMAGFSLSGAMFSTWRVHSITDLKLNKKVTKDYQOLPMVGVLLAIDIAIITWQ 582
DB 557 twilitvgytafagmfaktwrvaifknvkmkklkdkllivivggmllidclilicwq 616
QY 583 IADPFYR--ETKQLEPLHHEID----DVLVIPENYEQSEHMTIFVSIYAYKGLLLVF 636
DB 617 avdplrtvekysmep-----dpagrdisirpllehcenhtmtiwlgiyaykglmlif 670
QY 637 GAFLAWETHRHSIPALNDSKHIGFSVYVWFTCLAGAAISVLSDRKDLVFLVLLSFIIF 696
DB 671 gcfawetrnysipalndskeyigmsvynvglmciigaavsfldrdqpnvgfcilvailif 730
QY 697 CTTATCLVFPKVLKLRNPQGVV-DKRVATLRPMKNGRRDSSVCELEQ-----RLRD 751
DB 731 cstitclvfpkklitrtnpdaatqnrfqftqpkkedststsvtnqastsrleg 790
QY 752 VKNTNCRPKALMEKENEILQIRKL--GPEARKWIDVTCRGGSNVSGSELEPILNDDIV 809
DB 791 lqsenhrilrmkildkdeevtmqlqdtpekttyik-----qnhycelndiln---- 839
QY 810 RLSAPPVREMPSTTVTEMT--SDVSVTSTHVEMDNSFVSQVSTWAPSLPPPKKKQSIVE 866
DB 840 -----lgnftestdgkailknhldqn-----pq1-----q 865

QY 869 HHSHAPAPTMQPIQQ-QLQHHLQQHQHQMQQHHLQQQQHQHQMQQOQQOHHHHHLEKRN 927
DB 866 wnttepsrtckdpiedinspehiqrslslqpll-----hhaylpsig 908
QY 928 SVSA 931
DB 909 gvda 912

RESULT 5

AA51928
ID AAY51928 standard; Protein; 941 AA.

XX AC AAY51928;

DT 22-JUN-2000 (first entry)

XX Human GABA-B receptor protein.

DE GABA-B receptor; neuroprotectant; gene therapy; central nervous system;
KW metabotropic receptor; signal transduction; epilepsy; stroke; migraine;
KW psychological disease; stress; manic depression; schizophrenia; human.

XX Homo sapiens.

XX DEL9841941-AL.

XX 16-MAR-2000.

XX 14-SEP-1998; 98DE-1041941.

XX 14-SEP-1998; 98DE-1041941.

XX (BADI) BASF-LYNX BIOSCIENCE AG.

XX Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;

XX WPI: 2000-257875/23.

XX N-PSDB; AA289485.

XX A novel metabotropic receptor complex from the central nervous system,
PT related coding sequences and methods of identifying binding substances,
PT ligands and interactions with other proteins

XX Claim 1; Page 26-29; 32pp; German.

XX This invention describes a novel protein heteromer, containing at least
CC a GABA-B receptor protein and at least a protein (A) or its derivative
CC which retains the biological activity of the protein heteromer. The
CC protein of the invention has neuroprotective activity and can be used
CC for gene therapy. (A) or the protein heteromer are useful for identifying
CC proteins (or nucleic acids encoding such proteins) that show specific
CC binding affinity to (A) or the protein heteromer. The two-hybrid system
CC or biochemical methods can be used to identify interaction domains of
CC metabotropic receptors and use for pharmacotherapeutic intervention.
CC Structural information from the protein or protein complex is useful for
CC identifying and manufacture of substances which have specific binding
CC activity to the protein or protein complex. The protein heteromer and (A)
CC or fragments of these are useful as antigens to generate specific mono-
CC or polyclonal antibodies. The encoding nucleic acid (I) is useful for
CC identifying and isolating homologous sequences, as a marker for human
CC disease and for gene therapy. The methods can be used to identify
CC substances, which bind to (A) or (I) and that cause inhibition or
CC activation of functional effects of the GABAergic signal messages in
CC neurons of the central nervous system. The method can also identify
CC substances that inhibit or amplify interactions of (A) with other
CC metabotropic receptors or interaction of ligands with the protein
CC heteromer or (A) or interactions of (A) with G-proteins or other signal
CC transduction molecules. The analysis of the interactions of (A) and
CC GABA-B receptors is important for identifying potential active substances
CC against diseases such as epilepsy, stroke and psychological diseases such
CC as stress, manic depression, schizophrenia, migraine and others. This

CC The present sequence represents a human gamma-amino-butyric acid (GABA)
CC B receptor (GABABR) subunit designated HG20. The present invention
CC also describes the GABABR subunit designated GABABR1a. Cells expressing
CC the new receptor subunits are useful for identifying GABABR agonists
CC and antagonists. HG20 proteins and their antagonists are useful for
CC inhibiting HG20 or GABABR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders.

XX Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 20; Length 941;
Best Local Similarity 37.3%; Pred. No. le-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLLFLLL-----WSTACGRTAKRS-DVYIAGFPFYGDVNSYTGRCVM 53
DB 19 pparllllllllppllapagawargappppsppplsmgmlptkevakgsigrvli 78
QY 54 PSYKALGHVNEHGKILANRLHMMWNTQCNAAGVGVKSFDDMMHSGPNKYMFLFGAACH 113
DB 79 pavelaieqrne-sillrpfldlrlydtecdnakgikafydaikypgnhlmvfgvcps 137
QY 114 VTDPIAKASHWHLTQLSYADTHPMFT-KDAPNFFRVVPSNAPRALLKEFNWTR 172
DB 138 vtsiaeslgwnlvqlsfaatpvladkkkypffrtvpsdnavnpaillklkhyqwr 197
QY 173 VGVNYNEPRYSLPHNHVADLAMEVEVVTQSFVNDVAESLKLREKVKRIRIILGNFNE 232
DB 198 vglitqdvrfsevrnditvlygedleidsfndpctsvkklkgndvriilgfdq 257
QY 233 HFARKAFCEAYKIDMGKRAYQWLIMATYSTDW-----NVTQDSECSVEETATALEGALIV 288
DB 258 nmaakvfccayeenmgyksygiwipgyepsweweqvhteansrclrnkllaamegyivg 317
QY 289 DLLPLSTGDIIVAGTADYELVEYDRLR-GTEYSRPHGYTDGIWAAALAIQV----- 342
DB 318 dfeplsksqiktisgktpqgyeyreynnkrgvgpskfhgyaydgivwiaktlgrametlh 377
QY 343 AEKREDLLTHFDYVRKDWESVFEALRNTSFEQVTGVPVRYNNERKANILINQOLGOME 402
DB 378 assrhqrgdfnydhtlgrlllnammetnffvgvgrnrgemgtikftqfqsrev 437
QY 403 KIGEYHSQKSHLDLSLQKPKVGTTPKDPKTLIYIEHSONVNPITYIVSASVIGVITIA 462
DB 438 kvceynavadtlei-indtirfgseppkdtiilelrlkisiplysilsaltilgmima 496
QY 463 TVFLAFNIKRYNORYIKMSSPHLNLIIVGCMITYLSIIFGLDITLSSVAAFPYICTAR 522
DB 497 safllfnknrqkllkmsspynmnlilggmlsyasafiflgldgstfvsektfetlctvr 556
QY 523 AWILMAGFSLFCAMPSKTRWVHSIFTDLKNKKVYKIDYQLFWVGVLLAIDIAIITWQ 582
DB 557 twltyvgytafagmfaktwrhaifknvkmkklidqkllvlgvgmllidcillcwq 616
QY 583 IADPFYR--ETKOLEPLHHEID----DVLVIPENECQSEHMTIFVSIYAYKGLLVF 636
DB 617 avdplrrtvekysmep-----dpagrdisirpillehcenthmtiwigvaykgllmlf 670
QY 637 GAFLEWTRHVSIPALNDSKHGFSVYNVFITCIAGAAISLVLSDRKDLVFLVLSFFIIF 696
DB 671 gcflewetrnvsipalndskysigmvsynvgimcligaavsfltrdqpnvqfcivalvliif 730
QY 697 CITATLCVFPVKLVKRNPGQV-DKVRATLRPMKSKNGRDRSSVCELEQ-----RLRD 751
DB 731 cstitclvfpvkliitlrtnpdaatqnrrfftqngkedsktstsvtnvqaststrleg 790
QY 752 VKNTNCRFRKALMEKNEQLALIRKL--GPEARKWIDGVTCGSSNVGSELEPILNDDIV 809
DB 791 lqsenhrlrmkicelcdleevtnmqldtpekttyik-----qnhyqelndlin---- 839
QY 810 RLSAPPVVRREMPSTTTEMT-SVDSVSTHVMENDNSFVSQSTVMAPSLPPKKKKQISIVE 868

DB 840 -----lgnftstdggkalknhldqn-----pql-----q 865
QY 869 HHSHAPAPTMPIQQ-QIQHQ 927
DB 866 whtpestrctkdpiedinspehiqrslslpil-----hbaylpsig 908
QY 928 SVSA 931
DB 909 gvda 912

RESULT 4

AAW90938

ID AAW90938 standard; Protein; 941 AA.

XX AC AAW90938;

XX DT 14-JUL-2000 (first entry)

XX DE Human GABA-B receptor protein.

XX KW GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor;

XX KW human disease marker; gene therapy; central nervous system; epilepsy;

XX KW stroke; psychological disease; stress; manic depression; schizophrenia;

XX KW migraine.

XX OS Homo sapiens.

XX PN WO200015786-A1.

XX PD 23-MAR-2000.

XX PF 11-SEP-1999; 99WO-EP06742.

XX PR 14-SEP-1998; 98DE-1041941.

XX PR 04-DEC-1998; 98DE-1056066.

XX PA (BADI) BASF-LYNX BIOSCIENCE AG.

XX PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;

XX DR N-PSDB; AAA11696.

XX WPI; 2000-283281/24.

XX PT A novel metabotropic receptor complex from the central nervous system,

XX PT related coding sequences and methods of identifying binding substances,

XX PS ligands and interactions with other proteins

XX XX Claim 5; Page 53-56; 66pp; German.

CC This invention describes a novel protein heteromer, containing at least
CC a GABA-B receptor protein and at least a protein (A) or a sequence which
CC has a substitution, inversion, insertion or deletion of one or more amino
CC acid residues and which retains the biological activity of the protein
CC heteromer and which has neuroprotective activity. The encoding nucleic
CC acid (I), the construct, (A) or the protein heteromer are useful for
CC identifying proteins (or nucleic acids encoding such proteins) that show
CC specific binding affinity to (A) or the protein heteromer. The two-hybrid
CC system or biochemical methods can be used to identify interaction domains
CC of metabotropic receptors and use for pharmacotherapeutic intervention.
CC Structural information from the protein or protein complex is useful for
CC identifying and manufacture of substances which have specific binding
CC activity to the protein or protein complex. The protein heteromer and
CC (A), or fragments of these are useful as antigens to generate specific
CC mono- or polyclonal antibodies. (I) is useful for identifying and
CC isolating homologous sequences, as a marker for human disease and for
CC gene therapy. The methods can be used to identify substances, which bind
CC to (A) or (I) and that cause inhibition or activation of functional
CC effects of the GABAergic signal messages in neurons of the central
CC nervous system. The method can also identify substances that inhibit or
CC amplify interactions of (A) with other metabotropic receptors or
CC interaction of ligands with the protein heteromer or (A) or interactions

[illegible]

Db	617	avdplrrtvekysnep-----dpagrdisirpillehcenthmtiwlivaykglmlf	670
Qy	637	GAFLAWETRHSVPALNDSKHIGFSVYNVEITCLAGAAISLVLSDRKDLVLLSFFLIIF	696
Db	671	gcflawetrnvspalndskylgmsvynvglmcligaavsfllrtdqpnvqfcivalviif	730
Qy	697	CTTATCLVFPKVELKRNPGQVV-DKRVKRALRPMKNGRRDSSVCELEQ-----RLRD	751
Db	731	csstlclvfpkltlirtpdaatqnrrfqftqkqkdkstsvtsvngqasterleg	790
Qy	752	VKNTNCRFRKALMEKENELQALIRKL--GPEARKWIDGVTTCTGGSNVGSLEPI	809
Db	791	lqsenhrllrmkldkdelevtmqlqdtpekttyik-----qnhyqelndilo----	839
Qy	810	RLSAPPVREMPSTTVEMT-SVDSVTSTHVEMDNSFVSQSTVMAPSLPPKKKSQIVE	868
Db	840	-----lgnftestdggkaillnldqn-----pql-----q	865
Qy	869	HHSAPAPTMQPIQQ-OLQOHLQHQOQOQHLQQOQHQOQOQOQOQHHRHLEKRN	927
Db	866	wnteprtckdpiedinspehiqrlslqlpl-----hhayl-----	904
Qy	928	SVSAQTDDNIGSITSTAGKRSGDCSSMRERROSTASRHYDGSQSTPTARPKYSSSHRNS	987
Db	905	-----pslggv-----dascvpcvpsptasprhrhv	930
Qy	988	STNISTSQSELSN 1000	
Db	931	ppsfrvmvsglsd 943	
RESULT 3			
AA	AY29796		
ID	AA29796	standard; Protein; 941 AA.	
AC	AA29796;		
XX			
XX			
DT	15-NOV-1999	(first entry)	
XX			
DE		Human gamma-amino-butyric acid B receptor subunit HG20.	
XX			
KW		Gamma-amino-butyric acid B receptor subunit; HG20; GABAB1A;	
KW		depression; epilepsy; neuropsychiatric disorder; dementia;	
KW		muscular contraction; central nervous system disorder.	
XX			
OS		Homo sapiens.	
XX			
PN		W09940114-A1.	
XX			
PD		12-AUG-1999.	
XX			
PF		03-FEB-1999; 99WO-US02361.	
XX			
PR		05-FEB-1998; 98US-0073767.	
XX			
PA		(MERI) MERCK & CO INC.	
PA		(MERI) MERCK FROSST CANADA INC.	
PA		(UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.	
PA		(USSH) US NAT INST OF HEALTH.	
XX			
PI		Bonner TI, Bonnert TP, Clark J, Kolakowski LF, Liu Q;	
PI		McDonald T, Ng GYK;	
XX			
DR		WPI; 1999-527300/44.	
XX		N-PSDB; AA206968.	
XX			
PT		New DNA encoding human and murine receptor subunits, useful for	
PT		identifying agonists and antagonists for treatment of depression,	
PT		epilepsy and neuropsychiatric disorders	
XX			
PS		Claim 7; Fig 2; 128pp; English.	
XX			

Claim 2: Page 32-39; 62pp; German.

This invention describes a novel polypeptide (I), functioning as a gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal activity. (I), also the nucleic acid (II) that encodes it and related vectors, host cells, antibodies and transgenic invertebrates, are used for identifying: (i) new plant protection agents, i.e. modulators of (I) with insecticidal activity, which may also be useful in human or veterinary medicine; and (ii) genes that encode polypeptides involved in assembly of functionally related GABA-B receptors in insects. This sequence represents a fruitfly (*Drosophila melanogaster*) GABA-B receptor which is described in the method of the invention.

Sequence 1220 AA;

```

Query Match      100.0%; Score 6409; DB 22; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFRPSWFPFASLLFLILWSTACGRKAKRSVDYTAGFFPYGDGVNSYTGKVPMSVKLAL 60
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 mfrpswfpfasllflilwstacgrkarsdvytagffpygdgvnsytgkvpmsvklal 60

QY 61 GHVNEHGKILANYRLHMMWNDDTCNAAVGVKSPFDMHSGPNKVMFLFGAACTHTDPIAK 120
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 ghvnehgkilanyrlhmmwnddtcnaavgvksffdmhsgpnkvmflfgaaacthvtdpiak 120

QY 121 ASKHWHLTQLSYADTHPMFTKDAFPNFRVVPSENAFNAPRALLLKFFNTRVGTVQNE 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 askhwhltqlsyadthpmftkdafpnfrvvpsefnapralllkffntrvgtvqne 180

QY 121 askhwhltqlsyadthpmftkdafpnfrvvpsefnapralllkffntrvgtvqne 180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 pryslphnmhvaddlamevevvetqspndvdaesllklrekdvriilngnehfarkafc 240

QY 181 PRYSLPHNMHVADDLAMEVEVETQSPNDVDAESLLKLREKDVRIILNGNEHFARKAFC 240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 pryslphnmhvaddlamevevetqsfndvdaesllklrekdvriilngnehfarkafc 240

QY 241 EAYKLDMYGRAYQWLIMATYSTDWNVNTQDSEKSVESIEATALEGAILVDLLPLSTSGDIT 300
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 eaykldmygrayqwlmatystdwnvntqdsesveieatalegailvdlplstsgdit 300

QY 301 VAGITADEYLVEYDRLRGTSEYSPHGTYDGIWAAALAIQYVAEKREDDLTHFDYRVKDW 360
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 vagitadeylveydrirgtseysfphgtydgiwaaalaiqyvaeekredllthfdyrvkdw 360

QY 361 ESVFLCALRNTSFEVGTGVPYRFYNNERKANILLNOLFQGWKIGEYHOKSHLDSLIGK 420
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
361 esvflcalrntsfevgtgvpfyrfyannerkanillnqfkgmekigeyhokshldsligk 420

QY 421 PVKWVGKTPPKDRTLIYIEHSQNPNTIYVSASASVIGVIAIVFLAFNIKYRNQRIKM 480
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
421 pvkwvgktpkdrtllyiehsqnpntiyvsasasvigviiatvflafnikyrnqrikm 480

QY 481 SSPHLNLIIVGCMITYLSIIFGLDFTLSSVAAPPYICTARAWILMAGSLSFGAMFSK 540
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
481 ssphlnlivgcmitylsiiifgltdftlssvaaipyictarawilmagslsfgamfsk 540

QY 541 TWRVHSIFDTLKLNVKIDYQLFMVGVLLADIAITITWQADPYRETQKOLEPLHHE 600
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 twrvhsifdtlklnvkidyqlfmvvgvlladialititwqadpyretkoleplhhe 600

QY 601 NIDDDVLVIPENECYQSEHMTIFYSIIYAYKGLLLVFGAFLAWETRHRVSIIPALNDSKHIGF 660
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
601 niddvlvipenecyqsehmtifysiiyaykgl llvfgaflawetrhrvsiipalndskhigf 660

QY 661 SVYNVFTITCLAGAAISLIVSDRKDLVFVLLSFFIIFCTTATLCLVFPKLVELKRNQGV 720
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
661 svynvftitclagaaaislivsdrkdlvfllsffiifcttatlclvfpklvelkrnpqgv 720

QY 721 VDKRVPRATLRPMKNGRRDSSVCELEQRLRDVKNTRCFRKALMEKENELQALIRKLIGPE 780
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
721 vdkrvpratlrpmkngrrdssvceleqrlrdvkntrcfrrkalmekenelqalirkligpe 780

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Qy	781	ARKWIDGVTCTCGSNVGSLEPILNDIDIVRLSAPPVRRMPSTTVTMTSDVSVTSTHVE	840
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Qy	841	MDNSPVSVOGVTWAPSLPKKKKOSTVEHHSHAPATMMQPIQQOOLQOHLQOHOQOQOH	900
Db	841	mdnsfvsgvgtwapslppkkkkgsivenhshapattmmqpiqqglqghlqghgmqgqh	900
Qy	901	LQQOQHOQOQOQOQOQHHRHLEKRNVSQAOTDDNIGSITSTAGKRSGGDCSSMRERRQ	960
Db	901	lqqqghgmqgqgqgqhhrhlekrrnvsqaotddnigsitstagrsggdcssmrerrq	960
Qy	961	STASHYDSGSGTOTPARPKYSSSHRNSSTNISTSQSELSNMCPSHSPSTPAVIKTPTASD	1020
Db	961	stashydsqsgtptarpkyssshrnsstnistsqselnmcphskpstpaviktpctasd	1020
Qy	1021	HRTSMGSAKSNFVVSOSDLWDHTLSHAKORQSPRYASPORCAEHGGHGMTYDNT	1080
Db	1021	hrrtsmgalksnfvvsqslwdhtlshakqrspnyasporcaehhghgmtydnt	1080
Qy	1081	TSPIQRVSSEKNRNKRPKPKGTVCQSETDSEERDDPPNSQPCVPQPKKYSRSSNIQHA	1140
Db	1081	tspiqrsvseknrnkhrpkpkgtvcqsetdseerddppnsqpcvpqrkysrssniqha	1140
Qy	1141	AHHSSPNVADPKQRSRGKODSIIYGASSSTELLEGETAILPIFRKLLTEKSPNYRGR	1200
Db	1141	ahhsspnvdpkqrsrgkqdsiiygassetellegetailpfrklltekspnygr	1200
Qy	1201	SAVGOSCPNISIKDIVEYL	1220
Db	1201	savgscpnisikdiveyl	1220
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AA	AY28837		
ID	AA	AY28837 standard; protein; 943 AA.	
XX	AA	AY28837;	
XX	AC		
XX	AC		
DT	DT	17-JAN-2000 (first entry)	
XX	XX	Human GABABR2 receptor protein.	
DE	DE		
XX	XX	Human GABABR2 receptor protein; human gamma-aminobutyric acid receptor;	
KW	KW	metabotropic receptor; synaptic transmission; antibody; spasticity;	
KW	KW	recombinant nucleic acid technique; motor control disorder;	
KW	KW	therapeutic modulator; GABABR2 quantification; affinity purification.	
XX	OS	Homo sapiens.	
OS	OS		
XX	XX		
FH	FH	Key Location/Qualifiers	
FT	FT	Misc-difference l3 /note= "Corresponds to cng codon"	
FT	FT	Misc-difference 942 /note= "No corresponding codon in seq ID no.1"	
FT	FT	Misc-difference 943 /note= "No corresponding codon in seq ID no.1"	
FT	FT	Domain 1..422	
FT	FT	/label= Extracellular_domain	
FT	FT	/note= "can be swapped with the portions of calcium receptor for measurement of antagonist activity"	
FT	FT	Domain 423..686	
FT	FT	/label= Transmembrane_domain	
FT	FT	Domain 687..883	
FT	FT	/label= Intracellular_domain	
FT	FT	/note= "can be swapped with the portions of calcium receptor for measuring intracellular effects"	
XX	XX		
PN	PN	W09951636-A2.	
XX	XX		
PD	PD	14-OCT-1999.	
XX	XX		
PF	PF	02-APR-1999; 99WO-US07352.	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 09:50:57 ; Search time 52.81 Seconds
(without alignments)
1711.218 Million cell updates/sec

Title: US-09-715-962-4

Perfect score: 6409

Sequence: 1 MFRPSWFPASLFLLLNST.....SAVQSCPNISIKDIVEYL 1220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6409	100.0	1220	22 AAB86160	D. melanogaster GA
2	1602	25.0	943	20 AAY28837	Human GABABR2 rece
3	1598	24.9	941	20 AAY29796	Human gamma-amino
4	1598	24.9	941	21 AA909038	Human GABA-B recep
5	1598	24.9	941	21 AAY51928	Human GABA-B recep
6	1598	24.9	941	21 AAY70328	Human GABA-B-R2 re
7	1598	24.9	941	21 AAY79202	Human GABAB recep
8	1598	24.9	941	21 AAY44342	Human 9b2 GABA B r
9	1598	24.9	941	22 AAB50088	HG20 protein seque
10	1597	24.9	941	21 AAY68743	A human gamma-amin
11	1596.5	24.9	914	21 AAY44344	Protein-1 related

12	1593	24.9	1303	20 AAY49132	GABA-BR2*Gqo5 fusi
13	1591.5	24.8	965	21 AAY44345	Protein-2 related
14	1590	24.8	898	20 AAY14082	Human GABABR2 prot
15	1590	24.8	898	21 AAY70326	Human gamma amino
16	1582.5	24.7	940	21 AAW90937	Rat GABA-B receptor
17	1582.5	24.7	940	21 AAY70327	Rat gamma amino bu
18	1581.5	24.7	940	21 AAY51927	Rat GABA-B recepto
19	1579.5	24.6	940	21 AAY14081	Rat 9b2 GABA B rec
20	1561	24.4	883	20 AAY14081	Rat GABABR2 protei
21	1442.5	22.5	859	20 AAY34111	Human GABA recepto
22	1442.5	22.5	859	20 AAY30311	Amino acid sequenc
23	1442.5	22.5	874	20 AAY29661	Human 7TM receptor
24	1249	19.5	659	22 AAB50094	GB2 protein. Caen
25	1229	19.2	1305	22 AAB86161	D. melanogaster GA
26	1186.5	18.5	840	22 AAB86159	D. melanogaster GA
27	1166.5	18.2	1323	20 AAY49133	GABA-BR1a*Gqo5 fus
28	1155.5	18.0	960	19 AAW40116	Rat GABA-BR1a rece
29	1155.5	18.0	960	22 AAB50089	Murine GABA-B-R1a.
30	1154.5	18.0	960	22 AAY29797	Murine gamma-amino
31	1154	18.0	962	22 AAB50090	Human GABA-B-R1a.
32	1152	18.0	844	19 AAW40118	Rat GABA-BR1b rece
33	1151.5	18.0	960	21 AAY83145	Human GABAB1A rec
34	1151.5	18.0	961	20 AAY28838	Human GABABR1a rec
35	1151.5	18.0	961	20 AAY29798	Human gamma-amino
36	1151.5	18.0	961	20 AAY14101	Human GABAB recep
37	1149.5	17.9	960	20 AAY28841	Rat GABABR1a recep
38	1149.5	17.9	960	20 AAY49122	Rat GABABR1a prote
39	1148	17.9	844	19 AAW40119	Human GABA-BR1b re
40	1148	17.9	844	20 AAY28839	Human GABABR1b rec
41	1148	17.9	844	20 AAY14102	Human GABAB recep
42	1148	17.9	844	21 AAY32467	Human G-protein co
43	1148	17.9	899	20 AAY14107	Human GABAB recep
44	1146	17.9	844	20 AAY28842	Rat GABABR1b recep
45	1146	17.9	844	20 AAY49123	Rat GABABR1b prote

ALIGNMENTS

RESULT 1
AAB86160
ID AAB86160 standard; Protein; 1220 AA.
XX
AC AAB86160:
XX
DT 03-AUG-2001 (first entry)
XX
DE D. melanogaster GABA-B receptor protein SEQ ID 4.
XX
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect.
XX
OS Drosophila melanogaster.
XX
PN DE19955408-A1.
XX
PD 23-MAY-2001.
XX
PF 18-NOV-1999; 99DE-1055408.
XX
PR 18-NOV-1999; 99DE-1055408.
XX
PA (FARB) BAYER AG.
XX
PI Raming K, Mezler M, Mueller T;
XX
DR WPI: 2001-318282/34.
DR N-PSDB; AAH20520.
XX
PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in
PT screening for potential insecticides, for plant protection or medicine,
PT also related nucleic acid

Query Match 4.48; Score 280.5; DB 2; Length 915;
Best Local Similarity 20.7%; Pred. No. 3.5e-15;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;

QY 7 FPFASLFLLLWSTACGRYAK-----RSDVYIAGFFP-YGDGVENSVTG-----RG 51
DB 16 FPCCVLEVLLCVLAAARGQEMAPHISIRIEGDVTIGGLFPVHAKGSPGCVPGDIKRENG 75
QY 52 V--MPSVKLALGHVNHGKILANYRLHMMWNTQCNAAVGKVFDDMMHS----- 99
DB 76 IHRLEAMLYALDQINSDPNLLPNTLGLARLDTCSRDTYALEQSLTFVQALIQKDTSDVR 135
QY 100 -----GPNKVM-LFGAACTHTDPTAKAKHHLTQLSYADTHPMFTKDAFPNFF 148
DB 136 CTNGEPPVFVKPEKVGIVGAGSSVIMVAILRLFIQIISYASTAPELSDRRYDF 195
QY 149 -RVVPSENAFNAPRLALKFENFTRVCTVYQNEPRYS----- 184
DB 196 SRVVPDSFQAQAMVDIVKALGWNYYSTL--ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKLREKDVRIILGNFNEHFA 235
DB 255 RIPQERKORTIDFDRIIKQLLDPNSRAVIFAND-----EDIKQIL----- 296
QY 236 RKAFCAYKLDWYGRAYQNLIMATYSTDWNVNQDSECSVEEITATALEGAILVLLPLST 295
DB 297 -----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGAIIQPKRATV 343
QY 296 SG-----DITVAGI---TADEYLVEYDRL-RGTEYS 322
DB 344 EGFDAVFTSRTLENNRNWFAFYEEENFNCKLTISGSKKEDTDKCTQGERIGKDSNYE 403
QY 323 RFHG-----YTYDGIWAAALAIQYVAEKREDLLTHFDYR--VKDWESV-----FLEALRNTSF 373
DB 404 Q-EGKVQFVIDAYAMAHALHM--NKLCA--DYRGVCPMEQAGCKLLKLYIRHNVF 457
QY 374 EGVGTG-PVRF-YNNERKANLLNQFQGMKEK-----IGEY--HSQKSHLDLSLGKPKVK- 423
DB 458 NGSAGTPVMFNKNGDAPGRYDIEFYQYQTTNTNPGYRLIGQWTDQLNIEDMQMGKGVRE 517
QY 424 -----WV-----GKTPPKDRT--- 434
DB 518 IPSVCTLPCKPQQRKKTGKTPCCWTCPCDGYQYQYQFDEMTQCQCPYDQRPENRTGCQ 577
QY 435 ---LIVIE-HSQVNPTIYVSASVIGVITATVF-LAFNLIKYNQRYIKMSSPHLANLI 489
DB 578 NPIIKLEWHS-----PWAVIPVFLMLG-IIATFVMTATFIRYNDTPIVRASGRELSYVL 632
QY 490 IVGCMITYLSIIFLGLDITLSSVAAFP--YICTARAWILMAGFSLSFCAFMSKTRVHSI 547
DB 633 LUGIFLCYI-ITEL-----MIAPDVAVCSFRRVFLGLGMCISYAALLTKTNRIYRI 683
QY 548 FTDLKLN---KKVIKDYQLFMVVGVLIAIDIAITTWQIADP-----FYRETKOLEPLHH 599
DB 684 FEQKKSVTAPRLISPTSQLAITSLSISVQLLGVFIWFGVDPNIIIDYDEHKTMP--- 740
QY 600 ENIDDLVLVIPENYCOSEHMTIFVSIYYAYKGLLVGAFANETRVHSIPALNDSKHIG 659
DB 741 EQARGVL-----KCIDTDIICSL--GYSILLMVTCTVYATKTRGP-ENFNEAKPIG 791
QY 660 FSVYNVFIITCLAGAAISLVLSDRKDLVFF--LISFFIIFCTTATLCLVFPKLVKLKRN 716
DB 792 FTWYTCIVWLAFIPIFFGTAQSAEKLYIQTTLTISMNLSASVALGMLYMPKYIIFH 851
QY 717 PQGVVDKRVRA-----TLRPMK-----NGRDSVCE 744
DB 852 PELNVQKRKRFRKAVVTAATMSSRLSHKPSDRPNGEAKTELCE 894

FILE: FBI
; ORGANISM: Homo sapiens
US-08-617-785-14

RESULT 11
US-08-617-785-12
; Sequence 12, Application US/08617785E

APPLICANT: FIOR, Peter J.
APPLICANT: Kuhn, Ranier

```

> APPLICANT: LINDAUR, KIRSTEN
> APPLICANT: PUTTNER, IRENE
> APPLICANT: KNOPFEL, THOMAS
> TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4
> TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
> FILE REFERENCE: 4-19679/A/PCT
> CURRENT APPLICATION NUMBER: US/08/617,785E
> CURRENT FILING DATE: 1996-03-19
> EARLIER APPLICATION NUMBER: PCT/EP94/02991
> EARLIER FILING DATE: 1994-09-07
> EARLIER APPLICATION NUMBER: EPO 9416553.7
> EARLIER FILING DATE: 1994-08-19
> EARLIER APPLICATION NUMBER: EPO 93810663.0
> EARLIER FILING DATE: 1993-09-20
> NUMBER OF SEQ ID NOS: 26
> SOFTWARE: PatentIn Ver. 2.0
> SEQ ID NO 12
> LENGTH: 915
> TYPE: PRT
> ORGANISM: Homo sapiens
> US-08-617-785-12

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Query Match	4.5%	Score	286.5	DB 4	Length	915
Best Local Similarity	20.8%	Pred. No.	1.1e-15			
Matches 196:	Conservative	144:	Mismatches	334:	Indels	269:
					Gaps	48:

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Qy	52	V--MPSVKLAGHVNEHGKILANYRLHMWNDDQCNAAVGVKSFFDMMHS-----99	
Db	76	IHRLEAMLYALDQINSPPNLLPNWTLCARILTDCSRDTVALEQSLSFTVOALLIQKOTSDVR	135
Qy	100	-----GPNKVM-LFGCAACTHYTDPIAKASKWHHLTQLSYADTHPMFTKDAPNPF	148
Db	136	CTNGEPVPVKPERKVGVIGVGSSVSIMYANTLRLFQPQISYASTAPELSDDRRYDFE	195
Qy	149	-RVYPSENAFNAPRLALKKEFNTRVGTVYONEPRYS-----184	
Db	196	SRRVPPDSFOQAAMDIVKALGNYYSTL-ASBGSYGEGKGVBSFTQISKXAGGLCIAQSV	254
Qy	185	-LPHNH--MVADLDAMEVEVETQS-----FYNDVAESKKLKREKDXRIILIGNFNEHFA	235
Db	255	RIPQRKDRITDFRIIKQLLDPNSRAVVIFAND-----EDIKQIL-----296	
Qy	236	RKAFCAYKLDMGVRAYOWULIMATYSTDMNVNTQDSECSEVEIATALEGAILVDLLPLST	295
Db	297	----AAAKRADOVGH-FLWV-----GSDSGMSKNPLPHOHEDIA-----EGAITOPKRATV	343

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: TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
: TITLE OF INVENTION: IDENTIFYING COMPOUNDS ACTIVE AT
: TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
: TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
: TITLE OF INVENTION: TREATMENT OF NEUROLOGICAL DISORDERS
: TITLE OF INVENTION: AND DISEASES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: Storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: FastSeq for Windows 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,289A
: FILING DATE: July 25, 1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/001,526
: FILING DATE: July 26, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 220/004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1056 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Protein
: US-08-687-289A-8

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Query Match	4.6%	Score 295.5;	DB 2;	Length 1056;
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QY	106	-----LFGAACTHVTDPIAKASKHWHLTQLSYADTH-PMETKDAPFNFRVVPVSENA	156
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Db	270	FDRLLRKLRELPLKARVV-----CFCEGMTVRGLLSAMRELGVVGE-----FS	313
QY	259	TYSTDWNVNTQDSECSVEEIAATALEGAILVDL-----LPIUSTSGDITVACI	304
Db	314	LIGSDGW---ADRDEVIYEVEPANGGITIKQLQSPSVRSFYDDYFKLRDLDTN-----	362

TITLE OF INVENTION: AND DISEASES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/687,289A
 FILING DATE: July 25, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/001,526
 FILING DATE: July 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 220/004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1219 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-687-289A-6

Query Match 4.6%; Score 297; DB 2; Length 1219;
 Best Local Similarity 18.3%; Pred. No. 2.1e-16;
 Matches 247; Conservative 189; Mismatches 449; Indels 466; Gaps 59;

QY	12	LLFLLLWSTAC-----GRKAKRSDVYIAGFPYGDGVENS-----YTGRGV	52
Db	9	VLLALTWHTSAVCPDQRAQKKGDIILGLPFIHFGVAAKDQDLKSRPESVECIYRNGF	68
QY	53	--MPSVKLALGHVNERGKILANLYRLHMWNDDTCNA-----AVGVKS	92
Db	69	RWLQAMIFAIEEINSSPALLPNTLTGVRIEDT-CNTVSKALEATLSFVAQNKIDSLNDE	127
QY	93	FFDMHSGPNKVMFGAACHVTHDPTAKASKHHLTOLSYADHPMT-KDAFPNFRV	151
Db	128	FCNCSEHIPSTIAVVGTSVSTAVANLGLFYIPOVSYASSRLLSNKNQKSFRLTI	187
QY	152	PSNAFNAPLALLKFNTRVGVTVONEPRYSILPH-----	187
Db	188	PNDHQATAMADIEIFRNWNVTIAADDD-YRPGIEKFEAEERDIDFSELISQY	246
QY	188	-----NHMVADLDAMEVEVYVTSQSFNVDAESLKLKREKDV-----	223
Db	247	SDEEIQHVVEVQNSTAKVIVVFSSGPDLEPLIKEIVRNTCKIWLASEAWASSLIA	306
QY	224	-----RIILGNFNEHPARKA-----FCEAYKLDYMYGRAYOWLMATYSTDWNVTQDSEC	273
Db	307	MPQYFHVHVGGTIG--FALKAGQIPGREFLK-KVHPRK---SVHNGFAKEFWEET--FNC	358
QY	274	SVEEITALEGAILVDLL-----PLSTSGDITVAGITADEYLVEYD	314
Db	359	HLQEGA---KGPLVPDFTFLRGLHEESGDRFSNSTAFRLPCT-GDENISSV--ETPYIDYT	412

QY	315	RLRGTEYSRFHCYTYDGIWAALAIQ--YVAEKREDLLTHFD-----YRVKOWESVLEAL	368
Db	413	HLR-ISYN-----VYLAVYSTAHALQDIYTCIPGRGLFTNGSCADIKKVEAMQ--VLKHL	464
QY	369	RNTSEGVGTG-----PVRFYN-----N	385
Db	465	RHLNFTNMWGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVYVNYVYAKKGERLFIN	524
QY	386	ERKANILINQFQ-----LGOMEKI-----GEYHSOKSHLDL	416
Db	525	EEL--ILWSGFSEVPFNSRDCLAGTRKGIIEGEPTCCPECVCEPDEYSDETASAC	582
QY	417	SLGRPVKWKVK--TPPKORTLIYIEHSQVNPITYIVSASVIGVILATVFLAFNIKRN	474
Db	583	NKCPDDFWSENHTSCPIPVRYLEWSDIES---IIAFAFSLGILVTLFVLVLEVLRYD	639
QY	475	QRYIKWSSPHLNLIIVGCMITYLSIIFLGDLDTLSSVAAPYIC-----TARAWI	525
Db	640	TPVAKSSRELCYIILAG-----IFLG-----YVCPFTLIAKPTTTCYL	679
QY	526	--LMAGFS--LSFGAMFSKTRVHSIFTDLKLKKVKIKDYQLFM-----VVGVLALD	574
Db	680	QRLVLGLSSAMCYSALVTKTNRARIILAGSK--KICTRKPRFMSAWAQVILASILISVQ	737
QY	575	IAIITFQIADFPYRETROLEPHHENIDDLVIVIPENECOSEHMTIFVSIYAYKGLLL	634
Db	738	LTLVTLIIMEP-----PMPILSYPSIKEVYLI-----CNTSLGVVAPV--GYNGLLI	784
QY	635	VFGAFLAMETHRVHSIPA-LNDSKHIGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLSFF	693
Db	785	MSCTYYAEKTRNV--PANFNEAKYIAFTMTYTCIIWLAFAVPIYF-----GSNYKIITTCFA	838
QY	694	IIFCTATLCLVFPKVLKRNPOGVYDKVRATL-----	729
Db	839	VSLSVTVAGCMFTPKMYIIIAKP-----ERNVRSFTTSDVVRMVGDKLPCRNTFLN	894
QY	730	-----RPMKNGRRD--SSVCELEQRDVK--KNTNCRFRKALMEKENEL---QALIRKLG	778
Db	895	IFRRKKPGAGNANSNGKSVSWSEPGGROAPKQGHVWQRLSVHVKTNETACNTAVIKPLT	954
QY	779	PEARWIDGVCTGGS-----NVGSE-----LEPILNDDIVLSAPPVREMPSTTV	825
Db	955	KSYOGSGKSLTFSADASTKTLYNVEEEDNTPSAHFSPSPSPSMVHRRGPPVATTPP----	1010
QY	826	TEMTSDVSVTSHVDMNSFVSQSTVNAPSLPPKKKKQSVIEHSHAPATMMQPIQO--	884
Db	1011	-----LPPLTAETPLFLADSVIPKGLPPLPQO-----QFOQPPQPPQPP	1054
QY	885	-QLQOHLQ-----QHOOQOQOHLQOQOQ	906
Db	1035	KSLMDQLGVVTFNFGSGIPDFHVLAVLAGPCTPGNSLSRLYPPPPPPHQLQMLPLHLSTQ	1114
QY	907	QOQOQOQOQOQHHHRLKRNVSQAOTDNTGSTSTSTAGKSGGDCSSMR-----ERR	959
Db	1115	ESI-----SPGEDIDDDSERFKLLQEEFYERE	1142
QY	960	QSTASRHYDSCSQTPARPKYSSSHRNSSTNTSTQSELSNMCPSKSTPAVITPTAS	1019
Db	1143	GNTEDELEEBEDLPTA-----SKLTPEDSPAL-----TPPSP	1175
QY	1020	DHRRTSMGSKLNFVWSQSLMDWDTHTLSHA	1050
Db	1176	FRDSVASSGVSSPSS-PVSESVLCTPPNVTYA	1205

RESULT 9
 US-08-687-289A-8
 ; Sequence 8, Application US/08687289A
 ; Patent No. 5981195
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuller, Forrest H.
 ; APPLICANT: Krapcho, Karen J.
 ; APPLICANT: Hammerland, Lance G.


```

Db 70 EKIHRLEAMLYAIDQINKDPDLSNITLGVRIIDT-CSDRTYALEQSLTFVQALIEKDA 128
QY 94 FDM-----MHSQPNKVM-LFGAACTHTDPIAKSKHWHLTQLSYADTHPMFTKDAF 144
Db 129 SDVKCANGDPPIFTKPKDISGVICAAASSVIMVANILRFLKIPQISYASTAPELSDNTR 188
QY 145 PNFF-RVVPSENAPNRLALLKEFNWTRVGTQYQNEPRYS-----LPHNHVADLDA 196
Db 189 YDFFSRVVPDYSQAQAMVDIVTALGNVYSTL-ASEGNYGESGVEAFTQISREIGGVC 247
QY 197 MEVEVETQSFVNDVAESLKLRE-KDVRILGNFNEHFARKACEAYKLDYGRAQWL 255
Db 248 AOSQIPREPRGPEFEKIIRLLETPNARAVIMFANEDDIRILEAAKLNQSGH-FLWI 306
QY 256 IMATYSTDMWNTQDSECSVEETATALEGAILVLLPLSTSGD-----ITVAGITAD 307
Db 307 -----GSDSWGSKIAPVYQOEETA---EGA--VTILPKRASIDGDFRFRSRTLANNRN 356
QY 308 EYLVEY-----DRL-RGTEYSRFRH-----YTYDGIWAALA 338
Db 357 VFAEFWEENFCGLSGHGRNRSHTKCTGLERARDSSEYQ-EGKVQFVIDAVYSMA 415
QY 339 IOYVAEKREDLLTHFDYRVKDWESV----FLEALRNTSFEVGTG-PVRF-YNNERKANIL 392
Db 416 LH---NMHKDLCPGYIGLCPRMSTIDGKELLYIRAVNFGSAGTPVTFNENGDA 472
QY 393 INOFQL-----GOMEKIGEHYSKSHDLS-----LG 419
Db 473 IFQYQTNKSTEVKIGHWTNQ-LHLKVEDMOWAHREHTHPASVCSLPCKEGKRTKVK 531
QY 420 KPVKW-----YKTPPKDRT---LIYIEHSQVNPRIYVSASAS 455
Db 532 VPCWHCECEGYNQVDELSCELCPLDQRPNNMRTGCOLIPIIKLEWHSPWAVPVFA 591
QY 456 VIGVIATVFLAPNIRKYNORYIKMSPHLNLIIVGCMITYLSIIFGLDFTLSSVA 515
Db 592 ILGIIATFVIVTVFVRYNDPPIVRASGRELSYLLTGIFLCY-SITFLMI-----AAPD 644
QY 516 PYICTARAWILMAGFSLSFAMFSKTRVHSIFTDKLN---KKVIRDYQLFMVGVLLA 572
Db 645 TIICSRFRVFLGCMCFYSALTLTKRIHRIFFQGRKSVTAPKFSIPASQLVITFSLIS 704
QY 573 IDIAITITWOIADP-----FYRETKQLEPLHHEIDVILVINEYCOSEHMTFVSI 627
Db 705 VQLLGVFVFWVDPPIIIDIYGEQRTLDP---EKARGVL-----KCDISDLICSL-- 753
QY 628 AYKGLLLVFGAFLAWETRHVSIPALNDSKHIGFSVYVNFITCLAGAAISLVLSDRK 687
Db 754 GYSILLMVTCTVYAIKTRGVP-ETFNKAIPGFTWYTTCTIILWAFIPIFFGTAQSA 812
QY 688 V---LLSFFIIFCTTATLCLVFPVKLVKELKNPQGVDKVR-----ATL----- 729
Db 813 IQTTTLVSMLSASVSLGMLYMPKVYIIFHPQONVQKRKRSPKAVVTAATMSKLIQ 872
QY 730 ---RPMKNGRRDSSVCE 744
Db 873 GNDRP---NGEVKSELCE 887

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RESULT 6

US-08-604-298-1

: Sequence 1, Application us/08604298

: Patent No. 6084084

: GENERAL INFORMATION:

: APPLICANT: Stormann, Thomas M.

: APPLICANT: Simin, Rachel T.

: APPLICANT: Hammerland, Lance G.

: APPLICANT: Fuller, Forrest H.

: TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC

: TITLE OF INVENTION: GLUTAMATE RECEPTOR

: NUMBER OF SEQUENCES: 16

: CORRESPONDENCE ADDRESS:

```

: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: FastSeq for Windows 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/604,298
: FILING DATE: February 21, 1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 212/044
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 908 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: US-08-604-298-1

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Query Match

4.8%; Score 306.5; DB 3; Length 908;

Best Local Similarity 20.8%; Pred. No. 1.9e-17;

Matches 191; Conservative 158; Mismatches 350; Indels 219; Gaps 43;

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QY 4 PSWFFPSALLFLLWSTACGRTRAKR-----SDVIAGFFP-YGDGVENSYTG---- 49
Db 12 PCFFLLTAKFYWL-TWQRTSHQYAHISIRVDGDIILGGLFPVHAKGERGVPCGELAK 69
QY 50 -RGV--MPSVKLALGHVNEHGKILANYRLHMMWNTQCN-----AAVGVKSF 93
Db 70 EKIHRLEAMLYAIDQINKDPDLSNITLGVRIIDT-CSDRTYALEQSLTFVQALIEKDA 128
QY 94 FDM-----MHSQPNKVM-LFGAACTHTDPIAKSKHWHLTQLSYADTHPMFTKDAF 144
Db 129 SDVKCANGDPPIFTKPKDISGVICAAASSVIMVANILRFLKIPQISYASTAPELSDNTR 188
QY 145 PNFF-RVVPSENAPNRLALLKEFNWTRVGTQYQNEPRYS-----LPHNHVADLDA 196
Db 189 YDFFSRVVPDYSQAQAMVDIVTALGNVYSTL-ASEGNYGESGVEAFTQISREIGGVC 247
QY 197 MEVEVETQSFVNDVAESLKLRE-KDVRILGNFNEHFARKACEAYKLDYGRAQWL 255
Db 248 AOSQIPREPRGPEFEKIIRLLETPNARAVIMFANEDDIRILEAAKLNQSGH-FLWI 306
QY 256 IMATYSTDMWNTQDSECSVEETATALEGAILVLLPLSTSGD-----ITVAGITAD 307
Db 307 -----GSDSWGSKIAPVYQOEETA---EGA--VTILPKRASIDGDFRFRSRTLANNRN 356
QY 308 EYLVEY-----DRL-RGTEYSRFRH-----YTYDGIWAALA 338
Db 357 VFAEFWEENFCGLSGHGRNRSHTKCTGLERARDSSEYQ-EGKVQFVIDAVYSMA 415
QY 339 IOYVAEKREDLLTHFDYRVKDWESV----FLEALRNTSFEVGTG-PVRF-YNNERKANIL 392
Db 416 LH---NMHKDLCPGYIGLCPRMSTIDGKELLYIRAVNFGSAGTPVTFNENGDA 472

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; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-6PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-09422-19

Query Match          4.8%; Score 309; DB 5; Length 912;
Best Local Similarity 20.5%; Pred No. 1.2e-17;
Matches 188; Conservative 152; Mismatches 326; Indels 250; Gaps 41;

Qy 30 DVIYIAGFFP-YGDGVNSYTG-----RGV--MPSVKLALGHVNEHGKILANLYRLHMMWMD 81
Db 48 DITLGLFPVHGSGEGKACGLKEGHRLEAMLFALDRINNDPDLNPNITFGLARILD 107

Qy 82 TCNC-----AAGVKSFDDM-----MHSGPNKVM-LFGAACHTHVTDPIA 119
Db 108 T-CSRDTHALEOSLTFVRALIEKDGTEVRCGRGPPITIKPERVGVIGASGSSVIMVA 166

Qy 120 KASKHWHLTQLSYADTHPMFTKADPNPF-RVVPSPNAPNAPLALLKEFNTRVGTVIQ 178
Db 167 NILRLFKPIQISYASTAPDLSNRYDFSRVPSYDYOQAMVDIVRALKWNVYSTL-A 225

Qy 179 NEPRYSLPHNHMVADLDAMEVEVETQSFVND---VAESLKKLRE-----220
Db 226 SSGSYG-----ESGVEAFIOKRENGVGVCIQSVKIPREPKEGFEFKIIRLLE 274

Qy 221 -KDVRIILGNFNEHFAKFCBAYKLDMTGRAYQWILIMATYSTDMWNVTQDSCSVEEIA 279
Db 275 TSNARGIILIFANEDDIRRVEAARRANOTGHFF-WM-----GSDSWGSKSAPVRLLEEA 328

Qy 280 TALEGAILVDLLPLSTSG-----DITVAGITADEVLVEYDR---LRGTEY 321
Db 329 ---EGAVTILPKRMSVGRGDFRFSSTRLDNNRRNIRWFAEFEDNFCKLSRHALKKGSHI 385

Qy 322 SRFHG-----YTDGIIWAAALAIQYVAEKREDLLTHFDY-----355
Db 386 KCTNRERIGQDSAYEQEGKVQFVIDAVYAMGHALHAM-----HRDLCPGRVGLCP 436

Qy 356 RVKDNESV-FLEALNRTSEGVG-PVRF-YNNERKANILINQFOL-----GQMEKIGEYH 408
Db 437 RMDPDVGTQLKYIRNVNFSGIAGNPVTFNENGDPAGRYDIYQYLRNGSAEYKVIG---493

Qy 409 SOKSHLDLSLGGPKPVKVG-----426
Db 494 SMTDLHLRIER-MQWPGSGQQLPSICSLPCQGERKKTVKGMACCWCEPCTGYQYQV 552

Qy 427 -----KTPKDRFL-----IXIHSQVNPTIYVSASASVIGVITATVFLAFN-IK 471
Db 553 DRYCTCKTCYDMRPTENRTSCQPIVLEWSDSPWAVLPFLAVVG-IAATLFVVVTVFVR 611

Qy 472 YRNQRYIKMSSPHLNLIIVGCMTYLSIIFGLDPTTLSSVAAPFYICPARAWILMAGFS 531
Db 612 YNDTPIVKAASGRLSVLLAGIFLCYATFTFLMAEPDLGT-----CSLRRIFLGLGMS 664

Qy 532 LSGAMFSTKTRVHVFIFDCLKN---KKVIKDYQLFVWVGVLLADIAITITWQIADPF- 587
Db 665 ISYALLTKNRIYRIFEGGKRSVAPRFPISPASQIAITFILLISQLLGCYVNFVDPDSH 724

Qy 588 ----YRETQKLEPLHHE-----NIDDLVLIPENEYCQSEHMTIFVSIYAYKGLLAVFGA 638
Db 725 SWDFQDQRTLDPRARGVILKCDISDLSI-----CLIGYSMLLAVTCT 768

; 639 FLAWETRHVSIPALNDSKHIGFSVYVNVFITCLACAAISLVLSRDLVFEV---LLSFFII 695
; 769 VYAIKTRGV-ETFNEAKPIGFTMITTCIVWLAFIPFFGTSQSADKLYIQTITLTVSVS 827
; 696 FCTATATCLVFPVKLVELKRNPOGVVDKRVRA-----TLRPMK-----NGRRDS 740
; 828 LSASVSLGMLYMPKVIYIILFHPQNVKPKRSLKAVYTAATMSNKFQKGNFRNGEAKS 887
; 741 SVCE-LEQRLRDVKNT 755
; 888 ELCENLETPALATKOT 903

RESULT 5
US-08-823-110-1
; Sequence 1, Application US/08823110
; Patent No. 6077675
; GENERAL INFORMATION:
; APPLICANT: Stormann, Thomas M.
; APPLICANT: Simin, Rachel T.
; APPLICANT: Hammerland, Lance G.
; APPLICANT: Fuller, Forrest H.
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC
; TITLE OF INVENTION: GLUTAMATE RECEPTOR
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,110
; FILING DATE: March 24, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/604,298
; FILING DATE: February 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 224/259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-823-110-1

Query Match          4.8%; Score 306.5; DB 3; Length 908;
Best Local Similarity 20.8%; Pred. No. 1.9e-17;
Matches 191; Conservative 158; Mismatches 350; Indels 219; Gaps 43;

Qy 4 PSWFFPASLFLLLWSTACGRATAK-----SDVYIAGFFP-YGDGVNSYTG-----49
Db 12 PCFELLTAKFYWL--TMMQRTHSQEAHRIYDGDIIILGLFPLVHAKGVRGYPGCGELKK 69
Qy 50 -RGV--MPSVKLALGHVNEHGKILANLYRLHMMWMDTCN-----AAGVKSF 93
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Db	357	VWF	AEFWEENGCKL	SGHKKNSHKKCTGLERTARDSSYEQ	---BGKVOQFVIDAVYSMAVA	415
Qy	339	IQY	VAEKREDILLTHFDY	RVKDWESV----	FLEALRNTSFEQVGTG	416
Db	416	LH	---	NMHKDLCPGYIGLC	PRMSIIDGKELLGYTRAVNFNGSAGT	417
Qy	393	INQ	FOL----	GOMBKIGBYHQS	KSHLDLS-----	418
Db	473	IFQ	QITNKSTYK	VIGHWTNQ	---LHLKVEDQMAHREHTHPASVCSLPCKPGERKKTKVG	419
Qy	420	KPV	KW-----	-----	VGKTPPKDRT-----	420
Db	532	VPC	CHCERC	BEGYNYQVDELS	CELCPDLQDRPMNMTQCQLPIIKLEHSPWAPVFEVA	421
Qy	456	VIG	VIATVFLAF	NKIKYRNQRY	IKMSSPHLNNLIIGVCMITYLSII	422
Db	592	ILGI	ATTFTVIVT	PVRYNDTPIV	ASGRELGYVLVTGIFCY	423
Qy	516	PIY	CTARAWIL	MAGFSLFS	FGAMFCTKRVHVSIFITDLKLN	424
Db	645	TIIC	SFRFV	ELGMCFSYA	ALLKTKNRIHFRPQKKSVTAPKFI	425
Qy	573	IDAI	ITTWQIADP	-----	FYRETKQLEPLHENIDDV	426
Db	705	VOLL	GVFWFVVD	PHPIIIDY	GEQRTLDP-----	427
Qy	628	AYK	GILLV	FGAFLAWETH	SVIPALNDSKHIGFSYVNVFITC	428
Db	754	GY	SILLMTVC	TVYANKTRGP	---ETFN	429
Qy	688	V---	LLSPFI	IFICTAT	ICLVFVKELKRNPGVVDKVR	430
Db	813	IQTT	TLTVMSLS	SASVSLGMLYMP	KVYIIIFHPQNVQKRRSF	431
Qy	730	---	RPMSK	NGRRDSVCE	---LEQRLRDVKNT	432
Db	873	GNDR	---	NGEVK	SFELCSLEFNT	433

```

RESULT      4
PCT-US91-09422-19
; Sequence 19, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolfhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/626,806

```

Matches 335; Conservative 156; Mismatches 300; Indels 169; Gaps 21;

QY 8 PFASLLFLLL-----WSTACGTAKRS-DVYTAGFPYGDGVENSTGRGVM 53
Db 4 PPARLLLLLLPLLLPLAPGAWGARGAPRPPSSPPLSLINGMLPTKKEVAKSGIGRVL 63
QY 54 PSVKALGHVNEHGKILANRLHWNDDTCNAAVGVKSFDDMMHSGPNKVMFGAACH 113
Db 64 PAVELAIEQRNE-SLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGNHLMVFGVCPS 122
QY 114 VTDPIAKASHHHLTOLSYADTHPMFT-KDAFPNFFRVPFSENAFNAPRLALLKEFNWR 172
Db 123 VTSIAESLQGNVLQSPAATPVLADKKKYPFFERTVSDNVAVNPAILKLLKHQWR 182
QY 173 VGTYYQNEPRYSPLPHNMVADLAMEVEVVTQSFVNDVAESLKKLEKDVRIILGNFNE 232
Db 183 VGPLTQDVQRFSEVRNDLTGLVXGEDIEISDTESFSNDPCTSVKLLKNDVRIILGQFDQ 242
QY 233 HFARKAFCEAYKLDYCRAYQWLIMATYSTDMNVITQDSECSVEEITALEGALLVDLLP 292
Db 243 NMAKVFC----- 250
QY 293 LSTSGDITVAGITADEVLYEYDRLR-GTEYSRFGHYTDGIWAAALAIQVY-----AEKR 346
Db 251 -----CTPOYEREYNKRSGVSPKFGHYAYDGIWIAKTLQRAMETLHASSR 299
QY 347 EDLLTHFDYRVKDWESVLEALRNTSFGVTPVRFYNNERKANILINQFQGMKEIGE 406
Db 300 HQRIODFNVDHTLGRILNAMNETNFFGVGTQVVFNGERMGTIKFTQFQDSREVAVGE 359
QY 407 YHSQSHLDLSLCKPKVWCKTPPKORTLIYIEHSQVNPPIYIVSASVIGVIAIVFL 466
Db 360 YNAVADTLEI-INDTIRFQSEPPKDKTIIELQRLKISLPLYSILSALTILGIMASAF 418
QY 467 AFNIKRYQRYIKMSSPHLNNLIIVGCMITYLSIFGLDITLSSVAAPFYICTARAWIL 526
Db 419 FPNKRNQKLIKSSPYMNNLIILGMLSYASIFLGLDGSFVSEKTFETLCTVTRWIL 478
QY 527 MAGFSLSFGAMFSTKRVHSIFDILKLNKKVQYQLFMVGVVLLADIAIITTWQIADP 586
Db 479 TVGYTTFAGAMFAKTRVHAIFKNVNMKKIIKQDKLLVIVGGMLLIDLCILICWQAVDP 538
QY 587 FYR-ETKQLEPLHENID----DVLVIPENECQSEHMTIFVSIYAYKGLLVGFAFL 640
Db 539 LRTVEKYSMEP-----DPAGRDISIRPLEHCENTHMTIWLGIYVAYKGLLMFCFL 592
QY 641 AWETRHSVPALNDSKHIGFSVYVNFITCLAGAAISLVLSDRDLVFLVLLSFFIIFCTTA 700
Db 593 AWETRNVSPALNDSKYGNSVNVGIMCIIGAASVFLTRDQPNVQPCIVALYIIFCSTI 652
QY 701 TLCLVFPKLVKLKRNPGQVY-DKRVRAIRLPMKSKNGRRDSSVCELEQ-----RLRDYKNT 755
Db 653 TLCLVFPKLVKLRTNPDAATQNRRTQFTQNKKEKSTSTSVTSVNAQSTSRLEGQSE 712
QY 756 NCRFRKALMEKENELQALIKL--GPEARKWIDCVTCTGGSNVGSELEPIILNDIVRLSA 813
Db 713 NHRLRMKITELDKLEEVMTQLODTEPTKTYIK-----QNHQYQELNDILN----- 757
QY 814 PPVRREMPSTVTTEMT-SVDSVTSTHVEDMNSFVSQSTVMAPSLPKKKQSVIHHSH 872
Db 758 -----LGNFTSTDGKAILKLNLDQN-----POL-----QNTT 787
QY 873 APAPTMQPIQO-QLOOHLQOHOQOQOHLQOQOHOQOQOQOQOHHHRLHLEKRNVSVA 931
Db 788 EPSRTCKDPEDINSPEHIQRRLSLQIPIL-----HHAYLPSIGGVA 830

RESULT 2

US-09-183-253-4

; Sequence 4, Application US/09183253

; Patent No. 6043054

; GENERAL INFORMATION:

; APPLICANT: VAWTEK, LISA

;

..

s

RESULT 3

US-08-855-146-2

;

;

;

APPLICANT: STAMMERS, MELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-253-4

Query Match 12.0%; Score 768; DB 3; Length 332;

Best Local Similarity 46.6%; Pred. No. 4e-58;

Matches 151; Conservative 67; Mismatches 92; Indels 14; Gaps 5;

QY 353 FDYRVKDWESVLEALRNTSFGVTPVRFYNNERKANILINQFQGMKEIGEVHSOKS 412

Db 5 FNYTDHTLGRILNAMNETNFFGVGTQVVFNGERMGTIKFTQFQDSREVAVGEYNAVD 64

QY 413 HLDLSLCKPKVWCKTPPKORTLIYIEHSQVNPPIYIVSASVIGVIAIVFLAFNIKY 472

Db 65 TLEI-INDTIRFQSEPPKDKTIIELQRLKISLPLYSILSALTILGIMASAFLEFNKN 123

QY 473 RNQRYIKMSSPHLNNLIIVGCMITYLSIFGLDITLSSVAAPFYICTARAWILMAGFSL 532

Db 124 RNQRLIKMSSPYMNNLIILGMLSYASIFLGLDGSFVSEKTFETLCTVTRWILTVGYTT 183

QY 533 SFGAMFSTKRVHSIFDILKLNKKVQYQLFMVGVVLLADIAIITTWQIADPYR--E 590

Db 184 AFGAMFAKTRVHAIFKNVNMKKIIKQDKLLVIVGGMLLIDLCILICWQAVDPLRRTVE 243

QY 591 TKQLEPLHENID----DVLVIPENECQSEHMTIFVSIYAYKGLLVGFAFLWETRH 646

Db 244 KYSNEP-----DPAGRDISIRPLEHCENTHMTIWLGIYVAYKGLLMFCFLWETRN 297

QY 647 VSPALNDSKHIGFSVYVNV-FITC 669

Db 298 VSPALNDSKYIGMSVYVNVGIISC 321

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OM protein - protein search, using sw model

Run on: April 30, 2002, 09:52:02 ; Search time 26.74 seconds
(without alignments)
1026.702 Million cell updates/sec

Title: US-09-715-962-4
Perfect score: 6409
Sequence: 1 MFRPSWFPASFLFLLLWST.....SAVGQSCPNIKCDIVEYL 1220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442.5	22.5	859	US-09-183-253-2	Sequence 2, Appli
2	768	12.0	332	US-09-183-253-4	Sequence 4, Appli
3	311	4.9	908	US-08-855-146-2	Sequence 2, Appli
4	309	4.8	912	PCT-US91-09422-19	Sequence 19, Appl
5	306.5	4.8	908	US-08-823-110-1	Sequence 1, Appli
6	306.5	4.8	908	US-08-604-298-1	Sequence 1, Appli
7	305	4.8	912	US-08-617-785-2	Sequence 2, Appli
8	297	4.6	1219	US-08-687-289A-6	Sequence 6, Appli
9	295.5	4.6	1056	US-08-687-289A-8	Sequence 8, Appli
10	290.5	4.5	922	US-08-617-785-14	Sequence 14, Appl
11	286.5	4.5	915	US-08-617-785-12	Sequence 12, Appl
12	285.5	4.5	1056	US-08-687-289A-7	Sequence 7, Appli
13	281	4.4	867	US-08-617-785-4	Sequence 4, Appli
14	280.5	4.4	915	US-08-453-862-2	Sequence 2, Appli
15	280.5	4.4	915	US-08-452-734A-2	Sequence 2, Appli
16	280.5	4.4	915	US-08-176-401B-2	Sequence 2, Appli
17	280.5	4.4	915	PCT-US94-14989-2	Sequence 2, Appli
18	278.5	4.3	1212	US-08-660-148-5	Sequence 5, Appli
19	277	4.3	877	US-09-126-280-2	Sequence 2, Appli
20	276.5	4.3	1194	US-08-538-526-1	Sequence 1, Appli
21	268	4.2	877	US-08-407-875-2	Sequence 2, Appli
22	267.5	4.2	1180	US-08-660-148-2	Sequence 2, Appli
23	266.5	4.2	1212	US-08-486-270-10	Sequence 10, Appl
24	266.5	4.2	1212	US-08-367-264-10	Sequence 10, Appl
25	265.5	4.1	1079	US-08-485-588-8	Sequence 8, Appli
26	265.5	4.1	1079	US-08-484-565-8	Sequence 8, Appli
27	265.5	4.1	1079	US-08-480-751-8	Sequence 8, Appli

28	265.5	4.1	1079	2	US-08-943-986-8	Sequence 8, Appli
29	265.5	4.1	1079	3	US-08-353-784-8	Sequence 8, Appli
30	265.5	4.1	1079	3	US-08-484-719B-8	Sequence 8, Appli
31	264.5	4.1	1212	1	US-08-072-574-10	Sequence 10, Appl
32	261.5	4.1	1199	1	US-08-041-538-2	Sequence 2, Appli
33	261.5	4.1	1199	1	US-08-463-642-2	Sequence 2, Appli
34	261.5	4.1	1199	1	US-08-455-602-2	Sequence 2, Appli
35	261.5	4.1	1199	2	US-08-465-157-2	Sequence 2, Appli
36	261.5	4.1	1199	5	PCT-US91-09422-2	Sequence 2, Appli
37	258	4.0	905	1	US-08-072-574-2	Sequence 2, Appli
38	255.5	4.0	1180	1	US-08-486-270-8	Sequence 8, Appli
39	255.5	4.0	1180	3	US-08-367-264-8	Sequence 8, Appli
40	254.5	4.0	906	1	US-08-486-270-2	Sequence 2, Appli
41	254.5	4.0	906	3	US-08-367-264-2	Sequence 2, Appli
42	252.5	3.9	1180	1	US-08-072-574-8	Sequence 8, Appli
43	250.5	3.9	906	5	PCT-US91-09422-17	Sequence 17, Appl
44	249	3.9	1078	1	US-08-485-588-7	Sequence 7, Appli
45	249	3.9	1078	1	US-08-484-565-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-2

Query Match 22.5%; Score 1442.5; DB 3; Length 859;
Best Local Similarity 34.9%; Pred. No. 9e-116;

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Db 785 FLIGYTCLLAAICFFFAKSR--KLPENFNEAKFITFSMLIFFIWIWISFIPAYASTYGKF 842
QY 675 ISLVLSDRKDLVFLVLLSEFIIFFCTTATLCVFPKLVLPKRNPGVVDK----- 723
Db 843 VSAV-----EVJAILAASFGLLA-----CIIFFNKIYIIILFKPSRNTIEEVRCSAAHAFK 892
QY 724 -RVRA TLPRMSKNGRSDSSVCELEQRLRDVKNTRCNFRKALMEKENELQALIRKLGPPEAR 782
Db 893 VAARATLRRSNVSRKRSSL----- 912
QY 783 KWIDGVTCTGGSNVSGELEPIILNDDIVRLSAPPVRRMPSTTVMETSVDSVTSTHVEMD 842
Db 913 -----GGSTGS-----TPSSSISS----- 926
QY 843 NSFVSVQSTVMAPSLPPKKKOSIVEHHISHAPATMMQPIQOOLQOHL---QQHQOQOQ 899
Db 927 -----KSNSEDPFP---RPERKQOQOPLALTQOEOQOQOPL 958
QY 900 HLOOQOHOQMO-----QQOQOQOHHHRHLEKRNVSVAQTDDNIGS 939
Db 959 TLPQOORSQOQPRCKQKQVIFGSGVTFTSLSFDEPOKNMAHRNSTHONSLEAQ----- 1011
QY 940 ITSTAGKRSBGDCSSMRERRQSTASRH-----YDSGSQTPTA---RPK 979
Db 1012 -----KSSDTLTHQPLLPLOCGETDLDLTQVETGLQGPVGGDORPE 1053
QY 980 YSSSHRNS-STNISTYSQS 996
Db 1054 VEDPEELSPALWVSSQS 1071
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QY 378 G-PVRF-YNNERKANILINQFL-----GOMEKIGEYHSQSKSHLDLSLGKPKVKGW-- 426
Db 449 GTPVMEENGADPRYDIFQYQATNGSASSGGYQAVQOW-AEALRLDMEV---LRWSGDP 504
QY 427 -TTPPKDRTL-----IYTE-----HSQ 442
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QY 443 VNPTIYI-----VSASAVIGVIAIVFLAFNIKYRNQRIYKMSPHLNLIIVG 492
Db 565 CRPTPVRLTWSSPWAALPLLALVIGMATTTIMATFMHRNDPIIVRASRELSYVLLTG 624
QY 493 CMITYLSIIFLGDLTTLSSVAAPP--YICTARAWILMAGFSLFGAMFSKTRVHSLFTD 550
Db 625 IFLIY-AITFL-----WAEPCAICAARLLGLGTLTYSALLTKYNIYRIFEQ 675
QY 551 LKLNKK-----VIKDYQLFMVVGVLAIADIAITWQIADP-----FYRETQKLEPHEN 601
Db 676 GKRSTVPPPEISPTSQLVITFG-LTSLQVVGVIAMLGAQPPHSDVIDYEQRTVDP---EQ 731
QY 602 IDDVIVIPENECQSEHMTIFVSIYAYKGLLLVFGAFLAWETHRVHSIPALNDSKHIGFS 661
Db 732 ARGVL-----KCDMSDLSLIGCL--GYSLLMVTCTVYAIKARGVP-ETFNEAKPIGFT 782
QY 662 VYNVEITCLAGAAISLVSDRKDLVFF--LLSFFIIFCTATLCLVFPKLVKLKRNQ 718
Db 783 MYTTCIINIAFVPIFGTAGSAKIIYIQTTLTVSLSASVSLGMLYVPRKYVILLFHP 842
QY 719 GVVDKRVRAFLR-----PMSKN 735
Db 843 QNVQKKRSLLKKTSTMAAPQONEN 866

RESULT 12
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5
A:Reference number: A42916; MUID: 92317054
A:Accession: A42916
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <ABE>
A:Cross-references: GB:D10891; PIDN:BAA01711.1; PID:dl002186; PID:g220814
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:107749, NCBI:107750)
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 4.0%; Score 256; DB 2; Length 1171;
Best Local Similarity 18.9%; Pred. No. 2.3e-07;
Matches 225; Conservative 154; Mismatches 381; Indels 428; Gaps 52;

QY 60 LGVNEHGKILAYRLHWMNDTQCNAAGVGVKSPFDMN----- 97
Db 76 LERINDPTLLPNITLCEITRDCSWHSVALEQSIERIDSLISSEEEGLVRCVDSGS 135
QY 98 -HSGPNKVMFLGAACTHTVDPIAKASHWHLTQLSYADTH-PMFTKDAFNFFRVVPSN 155
Db 136 FRSKKPIVGVIGPGSSSAIOVQNLQFNIPQIAYSATSMDLSDKTLFKYFMRVVPSDA 195
QY 156 AFNAPRLALLKEFNWTRVGTVYQNEPRYSLPHNHMWADLDAME-VEVVEYQSFVNDVAES 214
Db 196 QQARAMVDIVKRYNWTYVSVAHV-TEGNYGESGMEAFKDMSAKEGICIAHSYKIYSNAGEQ 254
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RESULT 13

A56715

calcium receptor (clone phpCar-4.0) - human

C:Species: Homo sapiens (man)

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QY 215 -----LKKLRE--KDVRIILGNFNEHFARKAFCEAYKLDIMYGRAYQWLIMATYSTDMWNV 267
Db 255 SFDKLLKLRSHLPKRVV-----ACFCE-----GMTVRGLIMA----- 288
QY 268 TQDSECSVEEATALEGAILVDLLPLSTSG-----DIT-----VAGITA----- 306
Db 289 -----MRRLGLAGE-----FLLGSDGWADRDVDTGQYQREAVGGITIKLQSPDKV 335
QY 307 -DEYLVEYD-----RLRG--TEYSRFE----- 325
Db 336 FDDYVYKLRPETNLRNPNWFQEFQHRFOCRLEGFAQENSKYKNTCNSSILTRTHHVQDSK 395
QY 326 -GYVDGTWAAALAIQYVAEK-----REDLLTHFDYRVKDWESVLEALRNTSFEQVT 377
Db 396 MGFVINAIYSMAYGHLNMQMSLCPGYAGLDCAMKPIDGR-----KLLDSLTKNTFTGVS 449
QY 378 GPVRFY--NNERKANILINQOLGOMEK-----IG-----EYHSQKSHLDL 416
Db 450 GDMILFDENGSPGRYEIMNFK--EMGRDYFDYINVGSNDGELKMDDEDEVWSKNNIIR 507
QY 417 SL-GKP-----VKWYGR-----TPPKDRTLIIYIEHS----- 441
Db 508 SVCSEPCKEGQIKVIRKEGVSOCWCTCPKENEYVDEYTCACQLGSWPTDGLTCDLI 567
QY 442 -----QVNPTIIVSASASVIGVITATVFLAFNIKYRNQRIYKMSPHLNLIIVG- 492
Db 568 PVQYLRWGDPEPIAAVVFACLGALLATLFTVTF--IIRDTPVVVKSSRELCTYILAGI 624
QY 493 -----CMIT-----YLSIIFLGDLTTLSSVAAPPYICTARAWILMAGFSLFGAM 537
Db 625 CLGYLCTELIAKPKQIYCYLQRIQIGLSP-----AMSYAL 661
QY 538 FSKTWRVHSIETDLKLNKKVTKDYQLFM-----VGVVLLAIDIAITWQIADPYRE 590
Db 662 VTKNRIARILAGSK--KKCTKKPRFMSACAQVIAFIIQIOLGIIVALFIMEP---- 715
QY 591 TKQLEPLH-HENIDDLVIPENECQSEHMTIFVSIYAYKGLLLVFGAFLAWETHRVHSI 649
Db 716 --PDIMHDYPSIREVYLI-----CNTTNLGVVTP--GYNGLLILSCTFYAFKTRNV-- 763
QY 650 PA-LNDSKHIGFSVYNVITCLAGAAISLVSDRKDLVFLVLSFFIIFCTTATLCLVFPV 708
Db 764 PANFNEAKYIAFTMYTTCIINIAFVPIYF--GSNYKIITMCFVSLSATVALGCMFVP 819
QY 709 KLVELKRNPPQGVVDKRVRAFLR-----PMSKNGRDRDSSVCELEQR----- 748
Db 820 KVIILARP-----ERNVRSFTTSTVVRMHVGDGKSSSAASRSSSLVNLKRRGSGSETL 875
QY 749 -----LRDVKNTN-----CRFKALMEKENELQ-ALIRKLGPEARKWIDGVTCTGG 793
Db 876 SSGKSVTWAOQNEKSTRGOHLWQRLSVHINKENPNQTAIVIKPFPKSTENRGPAAAGGG 935
QY 794 SNVGELEPILNDDIVRLSAPPVRREMPSTVTYEMTSVDVSTHVEMDNSFVSQSVTM 853
Db 936 SGPG--VAGAGNAGCATATGPG---EPPDAGPKALDY-----AEAESEFPA----- 976
QY 854 APSLPKKKKQOSIVEHHSHAPATMMQPTQQQLQQLHQHQHQHQHQHQHQHQHQ 913
Db 977 -----AARPRSPPLST----- 988
QY 914 QQQQHHHRLHLEKRNVSQAOTDDNIGSITSTAGKRSGGDCSSMRERRQSTASRHYDSGOT 973
Db 989 -----LSHLGASAGRTDDAPSLHSETAARSSSGSLMEQISSVVTRF----- 1032
QY 974 PTARPKYSSSHRNSNTNSTQSSELSNMCPSHKPSTPAVTKPTASDH 1021
Db 1033 -----TANI-----SELNSMM-LSTAATPGPGPICSSY 1061
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QY 23 GRTAKRS-----DVIYIAGFE-----PYGDGVENSYTR-----CV--MPSVKLALGHVN 64
Db 31 GASSRSVARMGDGVIIIGALFSVHHQPPAEKVPKCGEIREQYGIQVEMFHTLDKIN 90
QY 65 EHGKILANYRLHMMWNTDQCNAAGVKSFFDMH-----SGPNKVM----- 105
Db 91 ADPVLLNITLGSERISCHWSSVALQSIEFIRDSLISIRDEKDLNRLCPDGTLP 150
QY 106 -----LFGAACTHTYDPIAKASKHWHLTQLSYADTH--PMFTKDAPNFFRVVPSNA 156
Db 151 RTKKPIAGVIGPGSSVAIQONLLQLFDIPQIAYSATSIDLSOKTLYKFLRVVPSDTL 210
QY 157 FNAPRLALLKEFNWTRVGTVYQNEPRVSLPHNHHVADLDAME--VEVVTQSFVNDVAES- 214
Db 211 QARAMLDIVRYNNYTSYSAVH--TEGNTGESGMDAFKELAAQEGLCIAHSKDIYSNAGEKS 269
QY 215 ----LKKLREK--DVRILIGNFNEHFARKAFCEAY-----KLDYGRAYQWLIWA 258
Db 270 FDLRLKRLERLPKRVV-----CCEGNTVRGLLSAMRRRLGVGE-----FS 313
QY 259 TYSTDWNNVTQDSECSVEEIAATALEGAILVDL-----LPLSTSGDITVAGI 304
Db 314 LIGSDGW---ADRDVEIEGYEVEANGGITIKLQSPVRSFDDYFLKLRDLTN----- 362
QY 305 TADEYLYVEY-----DLRLG--TEYSRPH-----GYTYDGIWAAL 337
Db 363 TRNPFPEFWQHRFQCRPLGHLLENPNFKKYCTGNESLEENYVQDSKMGFYINAIYAMAH 422
QY 338 AIOVV-----AEKREDLLTHFDYRVKDWESVFLEALRNTSEFEGVTGPVRFYN 384
Db 423 GLQNNHALCPGHVGLCDAMKPIDGRKLLDFLIK-----SSFVGVSGEEWFD 470
QY 385 NERKA-----NILNQFQLQMEKIGEYHSQKSHLD--LSLCK----- 420
Db 471 EKGDPAGRYDIMNLIQYTEANRYDVYHVGTWHEGVNLIDDDYKIQNMKSGMVRSCVSEPC 530
QY 421 -PVKWKCK-----TPPKDRPLI-----YIEHSQ 442
Db 531 GOIKVRKGEVSCCWCITACKENEFVQDEFTCRACDLGWNPAELTGCEPIPVRYLEWSD 590
QY 443 VNPTIYIVSASVIGVITAFVFLAFNLIKRYNQRVIRKMSPHLNNLIIVGCMITVLSIIF 502
Db 591 IES---IIAIFSCGLHVLTVFLVFLVLYRDTVPVKSSRELVCYIIUAG-----IF 639
QY 503 LGLDTLLSSVAAFPYIC-----TARAWI--LMAGFS--LSFGAMFSKTRVHSTFT 549
Db 640 LG-----YVCPETLIAKPTTSCYLQRLVGLSSAMCYSALVTKTNRARILA 687
QY 550 DLKLNKKVVDYQLFM-----VGVULLAIDAIITWQIADFPYRETQLEPLHHENI 602
Db 688 GSK--KKICTRKPRFMSAWAQVILIASILISVQLTLVTVLTIIEP-----PMPILSYPSI 739
QY 603 DDVLVAPENECQSEHMTIFVSIIVAYKGLLVFGALFETWETHVSIIPA--LNDKSHIGFS 661
Db 740 KEVTLI-----CNTSNLGVAVP--GYNGLLIMSCTIYAFKTRNV--PANENAKYIATF 790
QY 662 VYNVFTCLAGAAISLSLSDKDLVFLVLLSFFIIFCTTATLCLVFVPLKVLKRNPGQV 721
Db 791 MYTTCIILWAFVPIYF---GSNKIITTCFAVSLSVTVLGCMTPKMYIIIAKP----- 842
QY 722 DKRVRAFL-----RPMKNGRRD--SSVCELEQRLRD 751
Db 843 ERNVSFAFTTSDVVRMHVGDGKLPGRSNTFLNIFRRKKPGAGNANSNGKSVSWSEPGGRQ 902
QY 752 V-KNTNCRFRKALMEKENEL-----QALIRKLGPEARKWIDVTCGTGS-----NVGSE-- 799
Db 903 APKQGHVWQRLSVHVKTNACQNTAVIKPLTKSYQSGSKSLTFSDAKTKLYNVEEDN 962
QY 800 -----LEPILNDDIVRLSAPPVRRPSTTVTEMTSVDSVTSTHVMNDNSFVSQSVTM 853
Db 963 TPSAHFSPSPSPSMVHRHGPVATTPP-----LPPLHTAEETPLFLADSVI 1009
QY 854 APSLPPKKKKQSIVEHSHAPAPMTMQPIQO--QLQOHLQ----- 891
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Db 1010 PKGLPPPLPQQ-----OPQQPPQPPQPKSLMDQLQGVVVTNFGSGIPDFHAVLAGP 1062
QY 892 -----HQOQMQOQHLOQOQHQQOQOQOQOQOQHHRHLEKRNVSQAQTD 934
Db 1063 GTPGNSLSLYPPPPPPQHQLQMLPLHLSTFQEESI----- 1097
QY 935 DNIGSITSTAGRSRGDCSSMR-----ERRQSTASRHYDSGSQTPTARPKYSSSHRNS 987
Db 1098 -----SPGEDIDDDSERFKLQOEFVYREGNTEDELEEEEDLPTA----- 1139
QY 988 STNISTSQSELNMCPSHPSKSTPAVTKTPTASDHRTSMGSKSNFVVSQSLDMDTHTPL 1047
Db 1140 -----SKLTPEDSPAL-----TPSPFRDSVASGSSVPSS--PVSESVLCTPPNV 1182
QY 1048 SHA 1050
Db 1183 TYA 1185

RESULT 11
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A46742
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate recepto
A:Reference number: A46742; MUID:93280152
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NA>
A:Cross-references: GB:D13963; NID:g391856; PIDN:BA03066.1; PID:g391857
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBIPI:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein
```

Query Match 4.0%; Score 258.5; DB 2; Length 871;
Best Local Similarity 19.9%; Pred.No.1.le-07;
Matches 184; Conservative 154; Mismatches 321; Indels 265; Gaps 44;

```
QY 12 LFLFLLLW----STACGRTAKR--SDVYIAGFFP-YGDGVENSYTG-----RGV--MPSVK 57
Db 8 LNLAWLWSQAGIACGAGSVRLAGGLTGLGLFPVHARGAAGACGALKKEQGVHRLAML 67
QY 58 LALGHVNEHGKILANYRLHMMWNTDQCN-----AAVGVKS 92
Db 68 YALDRVNADPELLPGVRLGARELDT--CSRDTYALEQALSFVQALLINGRGGDGEASVRCPG 126
QY 93 FDMHHSQPNK--VMLFGAACHTVDPTAKASKHWHLTQLSYADTHPMETKDAFNFF-R 149
Db 127 GVPPLRSAPPVRVAVGVASGSIMVANVRLFAIQISYASTAPELSDSTDDFSR 186
QY 150 VVPSNAFNAPRLALLKEFNWTRVGTVYQNEPRVSLPHNHHVADLDAMEVEVETQSFVN 209
Db 187 VVPPDSYQAQAMVDIVRALGWNVSTL-----ASEGNYGSGVEAF--VQISREAGGV- 237
QY 210 DVAESLKLRL-----KDVRIILGNFNEHFARKAFCEAYKLDYMTGRAYQ 253
Db 238 CIAQSIKIPREPCKPGEFHKVIRRLMETPNARGLIIFANEDDIRRVLEATRQANLGH-FL 296
QY 254 WLIMATYSTDWNNVTQDSECSVEEIAATALEGAILVDLLP----- 292
Db 297 WY-----GSDWSGSKISPIINLEEEAV---GAITI--LPKRASIDGFDQYFMTSRLENNR 346
QY 293 -----LSTSG---DITVAGITADEVLVE---YDLRGTEYSRFGHYTD 330
Db 347 RNINWFAEFWEENFNCKLTSSGQSDSTKRCTGEERIGQDSAYEQEGKVQ-----FVID 400
```

R:Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.

Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995

A:Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval

A:Reference number: A55594; MUID:95116508

A:Accession: A55594

A:Molecule type: mRNA

A:Residues: 1-133 'X' 135-1079 <RIC>

A:Cross-references: GB:U10354

A:Experimental source: kidney

C:Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:187-212/Region: hydrophobic

F:613-635/Domain: transmembrane #status predicted <TM1>

F:650-670/Domain: transmembrane #status predicted <TM2>

F:683-700/Domain: transmembrane #status predicted <TM3>

F:725-744/Domain: transmembrane #status predicted <TM4>

F:770-790/Domain: transmembrane #status predicted <TM5>

F:806-828/Domain: transmembrane #status predicted <TM6>

F:841-860/Domain: transmembrane #status predicted <TM7>

F:90,261,287,386,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #statu

F:794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict

Query Match 4.1%; Score 265.5; DB 2: Length 1079;

Best Local Similarity 18.0%; Pred. No. 5.5e-08;

Matches 224; Conservative 191; Mismatches 380; Indels 447; Gaps 56;

```
QY 13 LFLLLW-STACG---RTAKRSQVYTAGFFPYGDGVENS-----YTGRGV- 52
DB 10 LUALAWHSAYGPDQAQKKGDIILGGLFPIHFGVAAKDODLSRPSVEICIRNFRGR 69
QY 53 -MPSVKLALGHVNEHGKILANYRLHWMNDTQCN-----AVGVKSF 93
DB 70 WLQAMIFATEEINSFSLPNMTGLGYRIEDT-CNTYSKALEATLSFVAQNKIDSLNDEF 128
QY 94 FDMHSGPNKVMFLGAACTHTVDPIAKSKWHILTOLSTADTHPMT-KDAFPNFRVVP 152
DB 129 CMCSEHIPSTIAVGTGCVSTAVANLGLFLFYIPOVSAYASSRLLSNKNQYKSLRTIP 188
QY 153 SNAFNAPLALLKFNWTRVGTQVQNEPRYSILPHNHVADLDAME-----VEVVEQ 205
DB 189 NDEHOATAMADIEFRWNVGTGIAADDD-YGRPGIEKPRE-BAERDIDCDSSELISQY 246
QY 206 SFVNDVAESLKKLRKEDVRILILGNFNEHFAKFAECAYKLDYGRAYQWLIMATYST-- 262
DB 247 SDEETQOVVEVQIONSTAKVIVFSSGPDLEPLIKEIVRNITGRI--WLASEAWASSL 304
QY 263 -----DWNNVTQDSSEVVEE 277
DB 305 IAMPEYFHVVGCTIGFLKAGQITGPFREFLQKVHPRKSVHNGFAKEFEET--FNCHLQ 362
QY 278 IATALEGAILVD-----LLPLST-----SGDITVAGITADEVLVEYDLRGT 319
DB 363 GA---KGPLVPDVTFKVSHKEGGRNLLNSAFPLCTGDENINSV--ETPYMDYEHLR-I 416
QY 320 EYSRPHGVTYDGIWAALAIQ--YVAEKREDLLTHFD-----YRVKDWESVFLEALRNTSF 373
DB 417 SYN-----VYLAVYSTAHALQDIYCLPGRLFTNCSADIKKVEAWQ--VLKHLRLNF 469
QY 374 EGVTG-----PVRFYN-----NERKAN 390
DB 470 TNNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYNYAKKGBRLFINEEK-- 527
QY 391 ILINQF-----QLQGMEXI-----GEYH----- 408
DB 528 ILWSGFSREVFPFNSCRDQACTRKGIIEGPTCCFCEVCECPDGEYSGETDASACDKCPD 587
QY 409 ---SOKSHLDLSLGRPKVKKVGTTPPKDRTLIYIEHSONPTIIVSASASVIGVIATVF 465
DB 598 DFWSNENHTS-CIAKEIEFLATWEPGIAL-----TLF-----AVLGIFTAFV 630
QY 466 LAFNIKYRNQRIKMSSPHNLNLIIVGCMITY-LSIIFLGLDTTLLSSVAAPFYICTARAW 524
```

Query Match

Best Local Similarity 4.1%; Score 261.5; DB 2: Length 1199;

Matches 237; Conservative 183; Mismatches 440; Indels 463; Gaps 57;

Matches 237; Conservative 183; Mismatches 440; Indels 463; Gaps 57;

Matches 237; Conservative 183; Mismatches 440; Indels 463; Gaps 57;

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QY 765 EKENLQALIRK--LGPEAKWIDGVCTGGSNVSGSELEPIILNDDI-----VRLSAPP 815
Db 885 QHKEIECFTPKSGMG-----NGGRATMSSSNKSQSVTAQNEKSSRGQHLMQLSLIHI 937
QY 816 VRRMPSTTVTTEMTSDVSVTSHV-----EMDNISFVSQSTYMA-----PSLPP--K 860
Db 938 NKKENPQATAVIKPPKSTESRGLGPGRGAGSAGGVATGGAGCAGAGPGGPESPDAGP 997
QY 861 KKKOSIVVEHHSHAPAPTMQ---PIQQOQLQHLQHQHQOQOHLQOQOQOQOQOQO 917
Db 998 KALYDVAEAEHFPAPAPRPSPIST-----1024
QY 918 HHRHLEKRNVSQAQTDNIGISITSTAGKSGDCSSMRERQSTASRHYDSGQTPPTAR 977
Db 1025 -----LSHRAGSARTDDVPSLHSEPVARSSSOGSLMEQILSSVVTRF-----1068
QY 978 PKYSSSHRNSTNISTOSSELSNMCPSKPTPAYIKTPTASDHRRTSMGSAKSNFVV 1036
Db 1069 -----TANI-----SELNMLSTAAPSPGV-----GAPLCSYLI 1099

RESULT 8
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: J02132
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: J02131; MUID:94197696
A:Accession: J02132
A:Molecule type: mRNA
A:Residues: 1-1180 <MIN>
C:Comments: This protein is coupled to guanine nucleotide binding proteins.
F:580-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 4.2%; Score 270.5; DB 2; Length 1180;
Best Local Similarity 19.3%; Pred. No. 3.1e-08;
Matches 221; Conservative 145; Mismatches 343; Indels 439; Gaps 52;
QY 104 VMLFGAACHTVTDPIAKSKHWHLTQLSYADTH-PMFTKDAFPNFRVVPSENAFNAPRL 162
Db 144 VGVIGPGSSVAIQVQNLQLFNIPQIAYSATSMDLSKTLFKYFMRVVVPDQAQARAWY 203
QY 163 ALKEFNWTRVGTYYQNEPRYSLPHNHMVAIDLAME-VEVVTQSOFNDVAE-SLKKLRE 220
Db 204 DIVKRYNWTYYSAVH-TEGNTGESGMEAFKDMKAGICIAHSYKIYSNAGEQSFDKLLK 262
QY 221 KDVRIILGNFNEHFPAR-----KAFCEAYKLDYGRAYQLIMATYSTDWNNVTQDSECSVE 276
Db 263 K-----LTSHLPKARVYACFE-----GMTVRGLMA-----MR 291
QY 277 EIATALGAILVDLLPLSTSG-----DIT-----VAGITA-----DEYLVYED 314
Db 292 RLGLAGE-----FLLAGSDWADRYDVTGQYQREAVGGITIKLQSPDVKWFDDYLLKL 345
QY 315 -----RLRG--FEYSRFH-----GYTYDGIW 333
Db 346 PETNHRNPWFQEFQWHRFQRCLEGFPQENSKYKNTCSNLSLTKTHVYDSKMGFVINAII 405
QY 334 AAALAIQYVAEK-----REDLLTHFDYRVKDWESVFLEALRNTSFEGVTGPVRFY--N 384
Db 406 SMAYGLNMQMSLCPGVAGLGDAMKPIDGR-----KLLSLMKNTFTGVSGDTTLFDEN 459
```

```
QY 385 NERKANILINQOLGOMEK-----IG-----EYHSQKSHLDLSL-GKP--- 421
Db 460 GDSPGRYEIMNFK--EMGKDYFDYINVGSNDNGELKMDDEVMWKKSNIRSVCSPECK 517
QY 422 --VKWVGK-----TPPKDRTLIYIEHS-----Q 442
Db 518 GQIKVIRKEVSCCWTCTCKENEYVDEYTCACQOLGSWPTDDLTCGCDLIPVQYLWGD 577
QY 443 VNPITIVSASVIGVITATVFLAPNIKYRNORYIKMSPHLNNLIIVG-----C 493
Db 578 PEPIAAVFAEACLLATLFTVVF--IIRDTVPVVKSSRELCTILAGICIGLYCTFC 634
QY 494 MIT-----YLSIIIFGLDITLSSVAAAPPYICTARAWILMAGFSLSGFAMESKTRVHS 546
Db 635 LIAKPKQIYCIYQIRIGLSP-----AMSYALVTKTKTRIAR 671
QY 547 IFTDLKLNKKVKDYQLFM-----VVGVLIAIDIAITITWQIADPFVRETQKLEPLH- 598
Db 672 ILAGSK--KKICTKKPRFMSACAQIVIAFILICIQIIGIIVALEFMEP-----PIMHD 722
QY 599 HENIDVLVIPENECQSEHMTIFVSIYAYKGLLVFGAFLAWETHRVHSIPA-LNDSKH 657
Db 723 YPSIREVYLI-----CNTNLTGVTPL--GYNGLLISCTFYAFKTRNV--PANENEAKY 773
QY 658 IGFSVYNVEITCLAGAAISLVLSDRKDLVFLSFFIIFCTTATLCIVFVFKLVELKRN 717
Db 774 IAFMTYTTCIIWLAFFIYF--GSNYKIITMCFVSLSATVALGCMFVPKVYIILAKP 829
QY 718 QGVVDKRVKRTL-PMKNGRRDSSVCELEQR-----LRD----- 751
Db 830 -----ERNVRSATTSIVRMHVGDGKSSAAASRSSLVNLWKRSGSGETLRSNGKSVTW 885
QY 752 VKNTNC-----RPRKALMEKENELQALI-----RKLP--PARKWIDGVTC 791
Db 886 AQNEKSSRGQHLWQLRSIHNKENPQATVAKPPKSTESRGLGPGRGAGSAGVGAT 945
QY 792 GGSNVGSELEPIILNDDIVRLSAPPVREMPSTVTEMTSVDSVSTHVMDSNFSVQST 851
Db 946 GGAGCA-----GAGPGGPSPDA----- 963
QY 852 VMAPSLPPKKKQKQSIVEHSHAPAPTMQ---PIQQOQLQHLQHQHQOQOHLQOQOHO 908
Db 964 -----GPKALYDVAEAEHFPAPAPRPSPIST----- 992
QY 909 MQOQQOQQOHHHRLKRNVSQAQTDNIGISITSTAGKSGDCSSMRERROSTASRHYD 968
Db 993 -----LSHRAGSARTDDVPSLHSEPVARSSSOGSLMEQILSSVVTRF-- 1036
QY 969 GSGQTPAPRKYSSSHRSNSTNISTOSSELSNMCPSKPTPAYIKTPTASDHRRTSMGS 1028
Db 1037 -----TANI-----SELNMLSTAAPSPGV-----GA 1059
QY 1029 ALKSNEVV 1036
Db 1060 PLCSYLI 1067

RESULT 9
calcium/polyvalent cation-sensing receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I59362; A55594
R:Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
A:Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve
A:Reference number: I59362; MUID:95241465
A:Accession: I59362
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1079 <RES>
A:Cross-references: EMBL:U02089; NID:g790578; PIDN:AACS2195.1; PID:g790579
A:Experimental source: striatal
```


Db 799 PIFGTQAQSAEMVIOITTTITVSMKSLASVSLGMLYMPKVYIIIFHPBQNVQKRRSRFKA 858
QY 727 ----ATL-----RPMKNGRRDSSVCE-LBQRLRDVNT 755
Db 859 VVTAATMQSKLIQGNDRP---NGEVKSELCELSLETNTSSTKTT 899
RESULT 5
S71376
glutamate receptor homolog - cherry salmon
C:Species: Oncorhynchus masou (cherry salmon)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 01-May-1998
C:Accession: S71376
R:Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.
FEBS Lett. 392, 71-76, 1996
A:Title: Cloning and characterization of a bifunctional metabotropic receptor activated by glutamate
A:Reference number: S71376; MUID:96354880
A:Accession: S71376
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1218 <KUB>
C:Keywords: glycoprotein; phosphoprotein
F:603-625/Domain: transmembrane #status predicted <TM1>
F:640-660/Domain: transmembrane #status predicted <TM2>
F:672-690/Domain: transmembrane #status predicted <TM3>
F:717-737/Domain: transmembrane #status predicted <TM4>
F:761-782/Domain: transmembrane #status predicted <TM5>
F:796-817/Domain: transmembrane #status predicted <TM6>
F:826-850/Domain: transmembrane #status predicted <TM7>
F:104,233,403,525,757/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predicted

Query Match 4.6%; Score 297; DB 2; Length 1218;
Best Local Similarity 20.4%; Pred. No. 8.3e-10;
Matches 201; Conservative 153; Mismatches 336; Indels 294; Gaps 47;
QY 106 LFGAACHTVTDPIAKSKHWHLTQLSYADTH-PMFTKDAFFNFRVPSSENAFNAPRLAL 164
Db 169 VIGPGSSVAIQVQLLQLEFNIPQIAYSATSIDLSDKTLFKYFLRVPSDITLQARAILDI 228
QY 165 LKENWTRVGTVYQNEPRYSLPHNHVADLDAME-VEVETQSFVNDVAES-----LKKL 218
Db 229 VKRYNWTYVSVAHV-TEGNYGSGMEAFKELASQEGICIAHSDKIYSNAGERHFDLLRLKL 287
QY 219 REK--DVRITILGNFNEHFARAFCEAYKLDYGRAYOWLINA-----TYSTDW 265
Db 288 RERLPKARVV-----CFCE-----GMTVRGLLMAMRLGVAGFELLIGSDGW 330
QY 266 NVTDQSECSVEEIIATALEGAILVLLPLSTSGDITVAGITADEILVEY---DRLRGTEYS 322
Db 331 --ADRDEWVEGYQEAAGVITVKL---HSEEVIT---SFDDYFLKRLNLTNRNWPFP 379
QY 323 RF-----HGTYDGIWAAL-ALQYVAEKREDLLT 351
Db 380 EFWOHRQCRIPIGHPLENNMYRNKCSGYESLEDNYVDQSKMGFVINAITYAMAQGLHDMHS 439
QY 352 H-----FDYRKDWESVLEALRNTSFEQVGTG-----PVRF----- 382
Db 440 HLCPGHVLCKAMPDID-----GSQLEFLMRTSFTGVSQGVSDVWFDNGTTPGRIEIMN 493
QY 383 -----YNNERKANILINQQLGOMEXIGEYHSOKSHLDLSL-----GKP-----VKW 424
Db 494 LOYVEPGAFDYIN-----VGSNHEGOL-SIDDYMMQINRSDMWLSVCSEPCSGEIKV 545
QY 425 VGK-----TPPKDR-----TLIYIEHSQVNPFI 447
Db 546 IRKGEVSCCNWICTACKDNEIVODEFTCTACDLGNWPDPELEGCEPITLRYLEWGNPESIV 605
QY 448 YIYVASASVIGVITVFLAFNIYKRNQRYIKMSPHLNLIIVGCMITYLSIIFLGLDT 507

Db 606 QVVFV---CLGILVTSFVFIFFVLYRDTPVVKSSSRELVCYIIILAG-----IFLGYIC 654
QY 508 TLLSSAAFPYICTARAWILMAGES---LSFGAMFSKTRVHSIFDTDLKNNKVKTKDQLEFM 565
Db 655 PFTLIAQ-PTVASCYLQRLVLGLSATMCSYALVTKNRIARILAGSK--KKIKTRKPREM 711
QY 566 -----VVGVLIAIDIAITTWQIADPFYRETKQLEPLHHEIDDDVLVIPENEYCOSEH 618
Db 712 SAWAQLVIAGLLVSVQLTLEVTLLIILEP-----PMPVKSYPISIREVFLI-----CNTS- 759
QY 619 MTIFVSIYAYKGLLLVFGAFLAWETRHVSIPA-LNDSKHIGFSVYNVFTICLAGAAISL 677
Db 760 -TVGWAPLGYINGLLIMSTCYTFAKTRNV--PANFNEAKYIAFTMYTTCIWLAFPIYF 816
QY 678 VLSDRKDLVFLVLSFFIIFCTTATCLVFPVKLVEKLRNPQGVVDKRVRA-----TLRP 731
Db 817 ----GSNYKIITTSFVSLSVSVTVALGCMFSPIYIILAKP-----ERNVRSATFTSDWVRM 868
QY 732 MSKNGR---RDSVCELEQRLRDVKNTNCR-----FRKALMEKENELOAL-IRKLGP 779
Db 869 HVGDNVACRNSLLDMFKRKNSENKSVSWSEPPGARHHAPKGEHNWQRLSVHVHRQ 928
QY 780 EARKKIDWGTCTGGSNVSGSELEPILNDDIVRLSAPPVRRREMPSTTIVTMTSVDVSTSTHV 839
Db 929 EA-----GCSNQMAVIRPLTN-----TYHNTGSSMAFESDLSTKTLNV 968
QY 840 -EMDNSFVSQSVTMAPSL-----PPKKKQSIIVEHHSHAPAPTMQPIQQOOL 886
Db 969 ABEEDSDLVYRNPPLSPHMAHQINATTGGPMKEVDEVEVY-----PPVEHM 1018
QY 887 QOHLQHQHQWQOQ-----HLQOQO 905
Db 1019 PPHLPQSRVPIQQRVIMDHLQLOE 1042
RESULT 6
A49874
metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mglur7
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A49874; 157954
R:Okamoto, N.; Horii, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 c
A:Reference number: A49874; MUID:94117433
A:Accession: A49874
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric a
A:Reference number: 157954; MUID:94195260
A:Accession: 157954
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
C:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658
C:Genetics:
C:Gene: MGLUR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor
Query Match 4.4%; Score 280.5; DB 2; Length 915;
Best Local Similarity 20.7%; Pred. No. 5.4e-09;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;
QY 7 PPFASILLFLLNSTAGCRTAK-----RSDVYIAGFFP-YGDGVENSYTG-----RG 51
Db 16 FPCCVLEVLCLVLAARAGQEMYPAPHSIRIEGDVTIGGLFPVHAKGPGVPCGDIKRENG 75

Db 48 DITLGLFPVHGSGKAGKAGELKKEGTHRLLEAMLFALDRINNDPDLIPNITILGARILD 107
Qy 82 TQCNAAVGVKSFDDMMH-----SG-----PNKVM-LFGAACHVTDPPIAK 120
Db 108 TCSRTHALEQSLTFQALIELKDGTEVRGSGGPPIITKPERVVGIGAGSSVSITWAN 167
Qy 121 ASKHWHLTQLSVADTHPMETKDAFNPF-RVVPSENAFNAFLALKEFNWTRGVYQN 179
Db 168 ILRLFKIPQISYASTAPDLSNDRYDFFSRVPSDTPYQAQMWDIIVRALKNWTVSTL-AS 226
Qy 180 EPRYSLPHNHMVLADAMEVEVEVETQSFVND--VAESLKKLRE----- 220
Db 227 EGSYG-----ESVEAFIQKSRENGGVCIAQSKIPREPKYGEFKIILKLEET 275
Qy 221 KDVRILGNFNEHFARKAFCEAYKLDIMYGRAYQWILMATYSTDMNVTQDSECSVEEIA 280
Db 276 SNARGIILIFANEDDIRRVLEAARRANOTGHFF-WM-----GSDSWGSKAPVLRLEVA- 328
Qy 281 ALEGAILVDLLPLTSG-----DITVAGITADEYIVYDOR---LRGTEYS 322
Db 329 --EGAVTILPKRMSVRGDFRYFSRTLDNRRNINFAEFWEDNFHCKLSRHALKKGSHIK 386
Qy 323 RPHG-----YTDGIMAAALAIQVVAEKREDLLTHFDY-----R 356
Db 387 KCTNERIGQDSAYQEGKQVQVIDAVIANGHALHAM-----HRDLCPGRVGLCPR 437
Qy 357 VKDWESV-FLEALRNTSFGVTG-PVRF-YNNERKANILINQFQ-----GQMEKIGEYHS 409
Db 438 MDPVDGTQLLKIRNVNFGSIAGNPVTFNENGDAQGRYDIYQYQLRNGSAEYKVG---S 494
Qy 410 QKSHLDLSLGGKPVKVG----- 426
Db 495 WTDHLHLRIER-MQWPGSQQLPRISICSLPCQGERKTKVKGMACCWHCEPCPTGYQYQVD 553
Qy 427 ---KT-----PPKDRLL--IYIEHSQVNPITYIVSASVIGVLIATVFLAFN-IKY 472
Db 554 RYTKTKCPYDMRPTENRTSCQPIPIVKLEWSDSPWAVLPFLAVVG-IAATLFVYVVTFRY 612
Qy 473 RNQRYIKMSSPHLNLIIVGCMITYLSIIIFGLDTPTLSSVAAPPICTARAWILMAGFSL 532
Db 613 NDTPIVKASGRELVSIVLAGIFLCYATTFLMTAEPLGT-----CSLRIFELGMSI 665
Qy 533 SFGAMFSKTRVHVSIFTDLKLN---KKVIKDYQLFMVGVVLLAIDAIITWQIADPF-- 587
Db 666 SYAALLTKNTRYIRIPEQGRKSVSAPRFSIPASQALAITFILLSQLLGGICVWFVDPDPSHS 725
Qy 588 ---YRETKOLEPLHHE-----NIDDLVIVPENECYCOSEHMTIFVSIYAYKGLLVFGAF 639
Db 726 VYDFQDQRTLDPRFARGVYLKCDISLSLI-----CLLGYSMILLMTCTV 769
Qy 640 LAWETRHVSIPALNDSKHIGFVSYNVFIITCLAGAAISLVLSDRKDLVVF---LLSFFLIIF 696
Db 770 YAIKTRGVP-EFNEAKPIGFTWYTCIIVLAFIPIPIFGTSQADKLYIQTTTLTVSVSL 828
Qy 697 CTTATLCLVFPKVLKRNPGQWDRVRA-----TLRPMK-----NGRRDSS 741
Db 829 SASVSLGMLYMPKVYIILPHPEQNVKPKRSLKAVVTAATMSNKTQKGNFRNGEAKSE 888
Qy 742 VCE-LEQRLRDVANT 755
Db 889 LCENLETPALATKQT 903

RESULT 4

149142
metabotropic glutamate receptor 8 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I49142
R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory b
A:Reference number: I49142; MUID:95239344

A:Accession: I49142
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-908 <RES>
A:Cross-references: EMBL:U17252; NID:g854728; PIDN:AAA68149.1; PID:g854729
C:Genetics:
A:Gene: mclur8
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

Query Match 4.88; Score 305; DB 2; Length 908;

Best Local Similarity 20.7%; Pred. No. 1.8e-10;

Matches 195; Conservative 151; Mismatches 350; Indels 248; Gaps 42;

Qy 4 PSFPPFASLLFLILWSTACGRTAKR-----SDVYIAGFRP-YGDGVENSVTG--- 49
Db 12 PCFLLITAKFYWIL--TMMQTHSQEYAHSLRDLGDIILGLFPVHAKGERGVPCGDLKK 69
Qy 50 -RGV--MPSVKALGLHNEHGKILANYRLHMMWNTQCN-----AAVGKSF 93
Db 70 EKGHRLLEAMLIADQTNKDPDLLSNITLGVRIIDT-CSDRTYALEQSLTFVQALIEKDA 128
Qy 94 FDM-----MISGPNKVM-LFGAACHVTDPITAKSKHWHLTQLSYADTHPMFTDAP 144
Db 129 SDVKCANGDPPIETKPKDISGVIGAAAASSVIMVANTILRLFKIPQISYASTAPELSNTR 188
Qy 145 PNPF-RVVPSENAFNAFLALKEFNWTRGVYQNEPRYS-----LPHNHMVAIDLDA 196
Db 189 YDFSRVVPDPSYQAQMWDIIVTALGNVYSTL-ASENGYGESGVAEFTQISRIGVCII 247
Qy 197 MEVEVETQSFVNDVAESLKKLRE-KDVRILGNFNEHFARKAFCEAYKLDIMYGRAYQWL 255
Db 248 AQSQKIPREPFGCEFEKIIKRLLETPNARAVIMFANEDDIRGLEAAKKNQSGH-FLWI 306
Qy 256 IMATYSTDMNVTQDSECSVEEIALEGALLVDLLPLTSGD-----ITVAGITAD 307
Db 307 ----GSDSWGSKAPVYQVEEIA--EGA-VTILPKRASIDGFDYFRSRTLANNRN 356
Qy 308 EYLVEYDLRLCTEYSRPHG-----YTDGIMAAALAI 339
Db 357 VMFAEFSEGNFGKSGSHGKRNKSHIKCTGLERIARDSSYDEQGVQVFIIDAVYSMAIYL 416
Qy 340 -----QYVABEKREDLLTHFDYRVKDWESVLEALRNTSFGVTG-PVRF 382
Db 417 HNMHKLCPGYIGLCPRMVITIDGKELCY-----IRAVNFNGSAGTPVTF 461
Qy 383 -YNNERKANILINQFQOME---KIGEYHSQSKSHLDLS----- 417
Db 462 NENGDAQGRYDIFOYQINNKSTYKIIIGHWTNQLHLKVEDMQWANREHTHPASVCSLPCK 521
Qy 418 -----LGKPVKW-----VCKTPPKDRT-----LIVIE-HS 441
Db 522 PGERKTKVGVPCWCHGRCGECYQYVDELSCELCPDQDRPNINRTQCRPIIKLEWHS 581
Qy 442 QVNPTIVISASAVIGVLIATVFLAFNIIKYNQRYIKMSSPHLNLIIVGCMITYLSII 501
Db 582 ----PWAVPVLIALGLIATTFVITVFRYNDPIVPRASGRELVSIVLLTGIFLCY-SIT 636
Qy 502 FLGLDITLSSVAAPPICTARAWILMAGFSLSGFAMFSKTRVHVSIFTDLKLN---KKVI 558
Db 637 FLMI-----AAPDTIICSPPRIELGLCMCFSYAALLTKNTRIHRIFEPQGGKSVTAPKFI 690
Qy 559 KDYQLFMVGVVLLAIDAITWQIADP-----FYRETKOLEPLHNEIDDLVIVPENY 613
Db 691 SPASQLVITFSLISVQLLGVFVWFVDPDPTIIDYGEQRTLDP---ENARGVL-----K 741
Qy 614 CQSEHMTIFVSIYAYKGLLVFGAFIATWETRHVSIPALNDSKHIGFVSYNVFIITCLAGA 673
Db 742 CDISDLSLICSL--GYSLLMVTCTVYAIKTRGVP-EFNEAKPIGFTWYTCIIVLAFI 798
Qy 674 AISLVLSDRKDLVVF---LLSFFIIFCTTATLCLVFPKVLKRNPGQVVDKRVF---- 726


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QY 580 TWQIADPPFYRETKQLEPLHHENIDDLVLPENECQSEHMTIFVSIYAYKGLLLVFGAF 639
Db 723 TLIMEP-----PMPILSYPSIKEVYLI-----CNTSNLGVVAPL--GYNGLLIMSCY 769
QY 640 LAWETRHVSIPA-LNDSKHIGFSVNVFTCLAGAAISLVLSRDKDLVFFVLLSFFFIIFCT 698
Db 770 YAFKTRNV--PANFNEAKYIAFTMYTTCIIWLAFVPIYF-----GSNYKIIITTCFAVSLSV 823
QY 699 TATLCLVFVPKLVKLRNPQGVVD-----KRVRA TL 729
Db 824 TVALGCMFTPKMYIIIAKPERNVRSFTTSDVVRMHVGDGKLPSCRNTFLNIFERRKAGA 883
QY 730 RPMSKNGRRDSSVCELEQRLDY-KNTNCRFRKALMEKENEL-----QALIRKLGPEARKW 784
Db 884 GNANSNGK---SVSWSEPGGGQVPKGQHMWHRLSVHVKTNETACNQTA VIKPLTKSYQGS 940
QY 785 IDGVTCGGS-----NVGSE--LEPILNDDIVRLSAP-----PVRREMPSTVTWETSVD 832
Db 941 GKSLTFSDTSTKTLYNVEEEDAQPI-----RFSPPGSPSMVVRHVRVPSAATT----- 988
QY 833 SVTSTHVMENDSFVSQSTVMAPSLPPKKKQKQIIVEHHSHAPAPTMQPIQQOQQHQQ 892
Db 989 PLPLPHTAETPLFLAEPALPKGLPP-----PLQQQQQQPPPPQ 1027
QY 893 HQQMQQ 898
Db 1028 KSLMDQ 1033

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Search completed: April 30, 2002, 10:08:01
Job time: 188 sec

1	[1]	SEQUENCE FROM N.A.
2	RE	MEDLINE=96029774; PubMed=7476890;
3	RX	Desai M.A., Burnett J.P., Mayne N.G., Schoepp D.D.;
4	RA	"Cloning and expression of a human metabotropic glutamate receptor 1
5	RT	alpha: enhanced coupling on co-transfection with a glutamate
6	RT	transporter.";
7	RL	Mol. Pharmacol. 48:648-657(1995).
8	[2]	
9	SEQUENCE FROM N.A.	
10	RE	MEDLINE=97231349; PubMed=9076744;
11	RX	Stephan D., Bon C., Holzwarth J.A., Galvan M., Pruss R.M.;
12	RA	"Human metabotropic glutamate receptor 1: mRNA distribution,
13	RT	chromosome localization and functional expression of two splice
14	RT	variants.";
15	RL	Neuropharmacology 35:1649-1660(1996).
16	CC	-1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
17	CC	MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
18	CC	CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
19	CC	ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
20	CC	THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
21	CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
22	CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA (SHOWN HERE) AND BETA;
23	CC	ARE PRODUCED BY ALTERNATIVE SPLICING.
24	CC	-1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
25	CC	STRONGEST, TO MGLUR5.
26	-----	
27	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
28	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
29	CC	the European Bioinformatics Institute. There are no restrictions on its
30	CC	use by non-profit institutions as long as its content is in no way
31	CC	modified and this statement is not removed. Usage by and for commercial
32	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
33	CC	or send an email to license@isb-sib.ch).
34	-----	
35	EMBL; U31215; AAA87843.1; --	
36	DR	EMBL; U31216; AAA87844.1; --
37	DR	EMBL; L76627; AAB05337.1; --
38	DR	EMBL; L76631; AAB05338.1; --
39	DR	GCRdb; GCR_1825; --
40	DR	GCRdb; GCR_1826; --
41	DR	GCRdb; GCR_1982; --
42	DR	GCRdb; GCR_1983; --
43	DR	MIM; 604473; --
44	DR	InterPro: IPR001828; ANF_receptor.
45	DR	InterPro: IPR000337; GPCR_Mgr.
46	DR	Pfam; PF000003; 7tm_3; 1.
47	DR	Pfam; PF01094; ANF_receptor; 1.
48	DR	PRINTS; PR00248; GPCRMR.
49	DR	PRINTS; PR00593; MTABOTROPICR.
50	DR	PRINTS; PR01051; MTABOTROPICR.
51	DR	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
52	DR	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
53	DR	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
54	DR	PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
55	DR	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
56	KW	Multiene family; Alternative splicing.
57	KW	SIGNAL 1 18
58	FT	CHAIN 1 18
59	FT	CHAIN 19 1194
60	FT	DOMAIN 19 592
61	FT	TRANSMEM 593 615
62	FT	DOMAIN 616 629
63	FT	TRANSMEM 630 650
64	FT	DOMAIN 651 661
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66	FT	DOMAIN 681 706
67	FT	TRANSMEM 707 727
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70	FT	DOMAIN 773 785
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97	FT	TRANSMEM 815 840
98	FT	TRANSMEM 815 840
99	FT	TRANSMEM 815 840
100	FT	TRANSMEM 815 840

FT	DOMAIN	841	1194	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	1014	1035	GLN/PRO-RICH.
FT	DOMAIN	1067	1081	GLN/PRO-RICH.
FT	DOMAIN	1095	1130	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	1142	1194	SER-RICH.
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	515	515	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	887	906	NSNGKSVNSPGGGVKPG -> KKQPEFSPSQCPSAH
FT	VARSPLIC	907	1194	AQL (IN ISOFORM BETA).
FT	VARSPLIC	887	906	MISSING (IN ISOFORM BETA).
FT	CONFLICT	593	593	NSNGKSVNSPGGGVKPG -> KKQPEFSPSQCPSAH
FT	CONFLICT	593	593	VOL (IN ISOFORM BETA) FROM REF. 2).
FT	CONFLICT	593	593	P -> S (IN REF. 2).
FT	SEQUENCE	1194	AA; 132376	MW; 970E51AF40584F40 CRC64;
Qy	Query Match	4.3%	Score 276.5; DB 1; Length 1194;	
Qy	Best Local Similarity	19.2%;	Pred. No. 3e-08;	
Qy	Matches	220; Conservative	165; Mismatches	392; Indels 369; Gaps
Qy	2	FRPWFPPASLL-----FLLLNSTACGRTRAKR--SDVVIAGFF-----PYODGVENSYVT	48	
Db	8	FFPAIFLEVLSPRSGRKVLGAGSQRSVARMDGDVITGALFSVHHQPPAEKYPKRC	67	
Qy	49	GR-----GV--MPSVKLALGHVNEHGKILANYRLHMMWMDTCAAAVGVKSFEDMMH---	98	
Db	68	GEIREQGIQVRVEMFHTLDKINADPVLLPNITLGSIEIRDSCHWSVALEQSFIEIRDSL	127	
Qy	99	-----SGPNKVM-----LFGAACTHTDPIAKSKHHMLTOLSYAD	134	
Db	128	ISIRDEKGINRCLPDGOSLPPGRTKKPIAGVIGPGSSSVAIQVQNLQLQFDIPQAIYSA	187	
Qy	135	TH-PMFTKDAFPNFRVVPENAFNAPRLALKEFNWTRVGTVYQNEPRYSLPHNHVAD	193	
Db	188	TSIDLSDKTYKYFLRVVSDTTLQARMLDVKRYNWTYVTSAVH--TEGNYGESGMDAFKE	246	
Qy	194	LDAME-VVVVETQSFQNDVAES-----LKKLRK--DVRILIGNFNEHFAKAFCEAY--	243	
Db	247	LAAQEGICIAHSQKIYSNAGEKSFDRLLRLRLRPLKARVV-----CFCEGTVV	296	
Qy	244	-----KLDMYGRAYQWLIMATYSTDWNNVTQDSECSVEEYATALEGAILVDL----	290	
Db	297	RGLLSAMRRLGVGVE-----FSLIGSDG--ADRDEVIEGYEVEANGGITIKLQSPV	347	
Qy	291	-----IPLSTSGDITVAGITADEYLVEY-----DLRGTETYSRF-----	324	
Db	348	RSFDDYFLKRLDNT-----TRNPWFPEFQHRFOCRPLGHLLENPNFKRICTGNES	399	
Qy	325	-----HGYTDGIAAALAIQVV-----AKREDLLTHFDYRVKDWE	361	
Db	400	LEENVQDKMGFVINAITYAMAGLQNMHHALCPGHVGLCDAMPID-----G	447	
Qy	362	SVFLEALRNTSFGVGPVRFYNNERKA-----NILINQPLQGMKRGKIGEYHSQSHL	414	
Db	448	SKLLDFLIKSSFIVSGSEEWFFDEKDAFCRYDINMLQYTEANRYDYVHVGTWHEGVLINI	507	
Qy	415	D-----LSLQK-----PVK-----WV-----	425	
Db	508	DDYKIQMNKSGVRSVCSPEPLKQGIKVRKGVSCVCTACKENEVYQDEFTCKACADL	567	
Qy	426	GKTPPKDRT-----LIYIEHSONVTIYIVSNASVIGVITATVFLAFNIKYNQRVIK	479	
Db	568	GWPNADLTGCEPIPVRYLEWSNIEP-----IIAIAFSCGLIVTLFVTLFVLYRDTVPVK	624	
Qy	480	MSSPHLANLIIVGCMITYLSIIFGLDITLSSVAAPFYIC-----TARAWI--LMA	528	
Db	625	SSSRELCTIILAG-----IFLG-----YVCPFTLIAPPTTTSCHYLQRLIV	664	
Qy	529	GFS--LSFGAMFSKTRVHRSIFTDLKLNKVKIKDYQLEF-----VVGVLIAIDIAIIT	579	
Db	665	GLSSAMCYSAIVTKTNRIARILAGSK--KKICTRKPSPMSAAOVIATIASILISVOLTAV	722	

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CC EMBL; D28538; BAA05891.1; -
CC EMBL; D28539; BAA05892.1; -
CC EMBL; S64316; AAD13954.1; -
DR GCRdb; GCR_0761; -
DR GCRdb; GCR_1002; -
DR GCRdb; GCR_1003; -
DR GCRdb; GCR_1317; -
DR MIM; 604102; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01055; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1212
FT DOMAIN 22 579
FT TRANSMEM 580 602
FT DOMAIN 603 616
FT TRANSMEM 617 637
FT DOMAIN 638 648
FT TRANSMEM 649 667
FT DOMAIN 668 693
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FT DOMAIN 715 737
FT TRANSMEM 738 759
FT DOMAIN 760 772
FT TRANSMEM 773 795
FT DOMAIN 796 801
FT TRANSMEM 802 827
FT DOMAIN 828 1212
FT CARBOHYD 88 88
FT CARBOHYD 210 210
FT CARBOHYD 378 378
FT CARBOHYD 382 382
FT CARBOHYD 445 445
FT CARBOHYD 734 734
FT VARSPIC 877 908
SQ SEQUENCE 1212 AA; 132468 MW; A3C7360681C6A25 CRC64;

Query Match 4.3%; Score 278.5; DB 1; Length 1212;
Best Local Similarity 19.7%; Pred. No. 2.3e-08;
Matches 224; Conservative 157; Mismatches 369; Indels 389; Gaps 53;

QY 104 VMLFGAACHTVTDPIAKASKHHLTOLSYADTH-PMFTKDAFPNFRVPSENAFNAPRL 162
DB 144 VGVIGPGSSVAIQVONLQLFNIPQIAYSATSMDSKTLFKYFMRVPSDAQARAV 203

QY 163 ALLKENFTVRGVYQNEPRYSLPHNHVADLDAME-VEVETQSFVNDVAE-SLKKLRE 220
DB 204 DIVKRYNWTYVSAVH-TEGNYGESGMEAFKDSAKEGICIAHSKYIYNAGEQSFDKLK 262

QY 221 KDVRIILGNFNEHAR-----KAFCEAYKDMYGRAYQWLMATYSTDWNVNTQDSECSVE 276
DB 263 K-----LTSHPKARVVACFCE-----GMTVRGLLMA-----MR 291

QY 277 ETATALEGAILVDLLPLSTSG-----DIT-----VAGITA-----DEYLYEYD 314
DB 292 RLGLAGE-----FLLLGSDGWADRYDVTGQYQREAVGGITIKLQSPDKWFDYILKLR 345

QY 315 -----RLRG--TEYSRHF-----GYTYDGIW 333
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Db 346 PETNHRNPFOWFOHREFQCRLEGFPQENSKYKNTCNSSLTCLKTHHVQDSKMGFVINALY 405
QY 334 AAALAIQVAAEK-----REDLLTHFDYRVKDWESVLEALRNTSFECVGTGVPVRY--N 384
Db 406 SMAYGLHNQMSLCPGYAGLCDAMPIDGR-----KLLESLMKNTFTVSGDITLFDEN 459
QY 385 NERKANILINOLFOMEK-----IG-----EYHSQKSHLDLSL-GKP----- 421
Db 460 GDSPGRYEIMNFK--EMGKDFDYINVGSWNGELKMDDEVMWSKKNIIRSVCSPECK 517
QY 422 --VKWVGK-----TPPKDRTLIYIHS-----Q 442
Db 518 GQIKVIRKEVSCCWTCTPCKENEVYFDEYTCACQOLGSWPTDGLTCDLIPVQYLWGD 577
QY 443 VNPTIIVSASASVIGVIIATVFLAFNIKRYRQRYIKMSSPHLNLIIVG-----C 493
Db 578 PEPIAAVFAAGLLATLFTVTVF--IYRDTPVVSKSSRELICYIILAGICLYLCTFC 634
QY 494 MIT-----YLSIIFGLDITLSSVAAPFYICTARAWILMAGFSLSGFMSKTRVHS 546
Db 635 LIAKPKQIYCYLQRIIGLSP-----AMSYALVTKTNRAR 671
QY 547 IFTDLKLNKKVTKDYQLFM-----VGVLLAIDIAIITTWQIADPFYRETQKLEPLH- 598
Db 672 ILAGSK--KKICTKPRFMSACQLVIAFILIQILGIIVAFIMEP-----PDIMHD 722
QY 599 HENIDDLVIVPENECQSEHMTIFVSIYAYKGLLVFCGLAWETRHVSIPA-LNDSKH 657
Db 723 YPSIREVYLI-----CNTNIGVVTPL--GYNGLLILSTCTFYAFKTRNV--PANFWEAY 773
QY 658 IGFSYVNVFITCLAGAAISLVLSDRKDLVFLVLSFFIIFCTTATLCLVFPVKLVELKRN 717
Db 774 IAFWTYTCIIWLAFVPIYF-----GSNYKIITMCFVSLSATVALGCMFVPKVIILAK 829
QY 718 QGVVDKRVATLR-----PMSKNGRRDSVCELEQRRLRDVKNTNCRFR-KALM 764
Db 830 ----ERNVRSAPFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKR-RGSSGETLRYKDRRLA 884
QY 765 EKENELQALIRK--LGPEARKWIDGVTCTGSGNVSGSELEPILNDDI-----VRLSAPP 815
Db 885 QHKSIECTPKGSMG-----NGGRATMSSNGSKSVTWAQNEKSSRGQHLWQRLSIHI 937
QY 816 VREMPSTVTMTSVDVSPTS-----THVEMDNFSVSVQSTVMA-----PSLPP--K 860
Db 938 NKKEPNQTAIVIKPPKSTESRGLGAGACAGSGCVGATGGACGACAGCGGPGESDAGP 997
QY 861 KKKQSIVEHSHAPAPTMMQ-----PIQQQLQOHLQHQHQHQHQHQHQHQHQHQHQHQ 917
Db 998 KALYDVAEAEHFPAPARPSPIST-----1024

QY 918 HHRHLEKRNVSVAQTDDNIGSITSTAGKRGSGDCSSMRERROSTASRHYDSQSQTPTAR 977
Db 1025 ----LSHRAGASRTDDVPSLHSEPVARSSSQSGSLMEQISVVVTRF-----1068

QY 978 PKYSSSHRNSSTNISTQSSELNMCNCPHSPSTPAVTKTPTASDHRRTSMGSKLSNFV 1036
Db 1069 -----TANI-----SELNMLSLTAAPSPGV-----GAPLCSYLI 1099

RESULT 15
MGRL_HUMAN
ID MGRL_HUMAN STANDARD; PRT; 1194 AA.
AC Q13255; Q13256; Q14757; Q14758;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
GN GRM1 OR GPRC1A OR MGLUR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 591 615 I (POTENTIAL).
FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 628 648 II (POTENTIAL).
FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 655 675 III (POTENTIAL).
FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 703 723 IV (POTENTIAL).
FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 754 775 V (POTENTIAL).
FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 789 810 VI (POTENTIAL).
FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 826 850 VII (POTENTIAL).
FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 915 AA; 102231 MR; F28AFC4C6454A6C2 CRC64;

Query Match 4.4%; Score 280.5; DB 1; Length 915;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;

QY 7 PPFASLLFLLMWACGRGTA-----RSDVYIAGFFP-YGDGVNSVYTG-----RG 51
DB 16 FPCCVLEVLVLAARAAAGQEMAPHSIRIEGDTLGLFPVHAKGPGSGVPCGDIKRENG 75
QY 52 V--MPSVKLALGHVNEHGKILANYRLHMMWDTQCNAAGVGVKSPFDMHMS----- 99
DB 76 IHRLEAMLYADQINSDPNLNPVTLGARILDTCSRDTYALEQSLTFVQALIQKDTSDVR 135
QY 100 -----GPNKVM-LFGAACHTHTVDPIAKASKWHMLTQLSYADTHPMFTKDAFPNFF 148
DB 136 CTNGEPPVFKPKVGVGAGSSVSTWVANILFLFOIPQISYASTAPELSDRRYDF 195
QY 149 -RVVPSNAPNAPRLALKENFTRVGVYQNERYS----- 184
DB 196 SRVVPDSFQAQAMVDIVKALGNVYSTL-ASEGSGYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--WVADLDAMEVEVYETOS-----FVNDVAESLKKLEKDVRIILGNNEHFA 235
DB 255 RIPOERKDRITDFRIITKQLDTPNSRAVIFAND-----EDIKQL----- 296
QY 236 RKAFCEAYKLDWYGRAYOWLIMATYSTDMVNTQDSECSVEIATALEGAILVDLLPLST 295
DB 297 -----AAKRAQOVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGATIQPKRATV 343
QY 296 SG-----DITVAGI---TADYLVEYDRL-RGTEYS 322
DB 344 EGFDAYFTSRLNNRRNWFPAEYWEENFNCKLTISGSKKEDTDKCTGQERIGKDSNVE 403
QY 323 RFHG---YTDGIWAALATQYAEKREDLLTHFDYR---VKDWESV---FLEALRNTSF 373
DB 404 Q-EGKVQFVDVAYAMAHLMH---NKDLCA---DYRGVCPEMEQAGGKKLLKYIRHNF 457
QY 374 EGVYG--PVRE--YNNERRKANILINQFQGMKEK-----IGEY--HSQKSHLDLSLGGKPKV- 423
DB 458 NGSAGTPVMEKNKGDAFGRYDIFQYQTTNTNPGYRLIGQWTDQLQNLNEDMQWKGKGVRE 517
QY 424 -----WV-----GKTPPKDRT--- 434
DB 518 IPSSVCTLPCKPGORKKTKGTCTPCWTCPCDGYQYQFDEMTCQHCPCYDQRPNEHTCQ 577

QY 435 ---LIXIE-HSQVNPTIIVSASASVIGVIATVF-LAFNIKYRNQRYIKMSSPHLNNLI 489
DB 578 NIPILKEWHS---PWAVIPVFLAMLG-IATIEVWATPIRYNDTPIVRASGRELSTVL 632
QY 490 IVCMTIYLSIIIFLGLDITLSSVAAPF--YICTARAWILMAGFSLSGFAMFSKTRVHSHI 547
DB 633 LTGIFLCYI-ITFL-----MIAKPDVAVCSRRFVLGLGMCISVAALLTKTNRIYRI 683
QY 548 FTDKLN---KKVIXDYQLEWVGVVLLAIDIAIITTTQIADP-----FYRETKOLEPLHH 599
DB 684 FEQKKSVTAPRLISPTSQLAITSSVLGVLGFWGVDPPNIIIDYDHSKTMNP--- 740
QY 600 ENITDDVLVIPENEYQSEHMTIFVSIYAYKGLLLVFGAFLAWETRHVSIPALNDSKHIG 659
DB 741 EQARGVL-----KCDITDLOIICSL--GYSILLMVTYVVAIKTRGVP-ENFNEAPIG 791
QY 660 FSVYNVITCLAGAAISLVLSDRKDLVFV---LLSFFIIFCTTATLCLVFPVKLEVKRN 716
DB 792 FTWYTCIVWLAFIPFGTAQAEKLYIQTTTLTISNNLSASVALGMLYMPKVYIIFH 851
QY 717 PQGVVDKRVRA-----TLRPMK-----NGRRDSSVCE 744
DB 852 PELNVOKRKRKSFVAVVTAATMSSRLSHKPSDRPNGEAKTELCE 894

RESULT 14
MGR5_HUMAN
ID MGR5_HUMAN STANDARD; PRT; 1212 AA.
AC P41594;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR GPRC1E OR MGLUR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94197696; PubMed=7908515;
RA Minakami R., Katsuki F., Yamamoto T., Nakamura K., Sugiyama H.;
RT "Molecular cloning and the functional expression of two isoforms of
human metabotropic glutamate receptor subtype 5.";
RL Biochem. Biophys. Res. Commun. 199:1136-1143(1994).
RN [2]
RP REVISIONS.
RA Katsuki F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 860-952 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93343913; PubMed=7688218;
RA Minakami R., Katsuki F., Sugiyama H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon.";
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CHLORIDE CURRENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
32 RESIDUES.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLUR1.

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FT TRANSMEM 703 723 IV (POTENTIAL).
 FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 754 775 V (POTENTIAL).
 FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 789 810 VI (POTENTIAL).
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 826 850 VII (POTENTIAL).
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 433 433 Y -> F.
 FT FTID=VAR_003584.
 SO SEQUENCE 915 AA; 102250 MW; CFF94E06BF7F4919 CRC64;

Query Match 4.5%; Score 286.5; DB 1; Length 915;
 Best Local Similarity 20.8%; Pred. No. 5.6e-09;
 Matches 196; Conservative 144; Mismatches 334; Indels 269; Gaps 48;

Qy 7 PFPSALLFLLWSTACGRYAK-----RSDVYIAGFFP-YGDGVENSYTG-----RG 51
 Db 16 PFCCVLEVLCLALAAARQEMYPHSHIRIEGDTVLGLGFPVHAKGSPGVCDDIKRENG 75
 Qy 52 V--MPSVKLALGHVNEHGKILANYRLHMMNDTQCNAAVGVKSFDDMHHS----- 99
 Db 76 IHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDYVALEQSLTFVQALIQKDTSDVR 135
 Qy 100 -----GNKVM-LFGAACHTVTDPIAKSKWHLTOLSYADTHPMFTKDAFPNFF 148
 Db 136 CTNGPPVFKPKVGVGICAGSSVSIMVANILRLFIQPIQISYASTAPELSDDRYDF 195
 Qy 149 -RVVPSNAPRLALKKEFNWTRGVTVQVNEPRYS----- 184
 Db 196 SRVPPDSFOAAMVDIVALGNVYSTL-ASEGSTGKGVESFTQISKAGGLCIAQSV 254
 Qy 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKLREKDVRIILGNFNEHFA 235
 Db 255 RIPOERKORTIDFDRIKQLDTPNSRAVVIFAND-----EDIKQIL----- 296
 Qy 236 KFAFEAYKLDMYGRAYQWLIWATYSTDMNVNVDSECSVEETATALEGAILVDLLPLST 295
 Db 297 ----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA--EGAITIQPKRATV 343
 Qy 296 SG-----DITVAGI---TADVEIVEYDRL-RGEYS 322
 Db 344 EGFDAFTSRTLENRRNWFABYWEENFNCKLTISGSKKEDTRKCTGOERIGKDSNYE 403
 Qy 323 RFHG---YTDGIWAALAIQVAKREDLLTHFYR--VKDWESV---FLEALRNTSF 373
 Db 404 Q-EGKVQFVIDAVYAMAHALHM--NKDLCA--DYRGVCPMEQAGGKLLAYIRNVNF 457
 Qy 374 EGVTC-PVRF-YNNERKANILNQFOLGOMEK-----IGBY--HSOKSHLDLSLGRPKV 423
 Db 458 NGSAGTVMFNKNGDAPGRYDFIYQYTTNTSNPGYRLIGOWTDELQNLNIEDMOWGKVRE 517
 Qy 424 -----WV-----GKTPPKDRT--- 434
 Db 518 IPASVCTLPCKGQRKKTQKGFPCCTCPDCDGYQYQFDEMTCHQCPYDQRPENRTGCQ 577
 Qy 435 ---LIYIE-HSOVNPITYISASASVIGVITATVF-LAFNIKRYRNORYIKMSSPHLNLI 489
 Db 578 DIPIIKLEWHS---PWAVIPVFLAMLG-LIATIFVWATFIRINDPIVIRASGRELSTVYL 632
 Qy 490 IVGCMITYLSIIFLGLDITLSSVAAPP--YICTARAWILMAGFSLSPGAMFSTWRVHSI 547
 Db 633 LTGIFLCYI-ITFL-----MIAPDPAVAVCSFRFVRLGLGMCISVAALLTKTNRIYRI 683
 Qy 548 FTDLKLN---KKVIKDYQLFVWVGVLLAIDIAITITWQIADP-----FYRETKOLEPLHH 599
 Db 684 FEGGKSVTAPRLISPTSQLATITSSLISSVQLLGVFWFGVDPDPNIIIDYDEHKTMPN--- 740

Qy 600 ENIDDLVLPENEYCOSEHMTIFVSIIVAYKGLLLVFGAFLAWETRHVSPALNDSKHIG 659
 Db 741 EQARGVL-----KCDITDLQICSL--GYSILLMTCTVYAIKTRGVP-ENFNEAKPTG 791
 Qy 660 FSVYNVETCLAGAISLVSDRDLVFV---LLSFFIIFCTATLCLVFPVKLVKLKRN 716
 Db 792 FTYTTCVILWLAFLPIFFGTQSAEKLYIQTTLTISMNLSASVALGMLYMPKVYIIIPH 851
 Qy 717 PGVVVDRKVRV-----TLRPMK-----NGRRDSSVCE 744
 Db 852 PELNVQKRKRSFKAVVTAATWSSRLSHKPSDRPNGEAKTELCE 894
 RESULT 13
 MGR7_RAT
 ID MGR7_RAT STANDARD; PRT; 915 AA.
 AC P35400;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
 GN GRM7 OR GPRC1G OR MGLUR7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94117433; PubMed=8288585;
 RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
 RA Mizuno N., Nakanishi S.;
 RT "Molecular characterization of a new metabotropic glutamate receptor
 mGluR7 coupled to inhibitory cyclic AMP signal transduction.";
 RL J. Biol. Chem. 269:1231-1236(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
 RX MEDLINE=94117430; PubMed=8145723;
 RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
 RA Westbrook G.L.;
 RT "Cloning and expression of a new member of the L-2-amino-4-
 phosphonobutyric acid-sensitive class of metabotropic glutamate
 receptors.";
 RL Mol. Pharmacol. 45:367-372(1994).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D16817; BAA04092.1; -;
 CC EMBL; U06832; AAA20655.1; -;
 CC GCRDb; GCR_0945; -;
 CC GCRDb; GCR_0946; -;
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC Pfam; PF00003; 7tm_3; 1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC PRINTS; PR00248; GPCRMR.
 CC PRINTS; PR00593; MTABOTROPICR.
 CC PRINTS; PR01057; MTABOTROPICR.
 CC PROSITE; PS00979; G_PROTEIN_RECP_F3_1; 1.

RESULT 12

Db 832 NGEAKSELCELEAPALATKOT 903

RESULT 11

MGR_DROME

ID MGR_DROME STANDARD; PRT; 976 AA.

AC P91685;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR PRECURSOR.

GN GLURA OR GLU-RA.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

RP SEQUENCE FROM N.A.

RN STRAIN=OREGON-R;

RC MEDLINE=96421661; PubMed=8824309;

RA Parentier M.L., Plin J.P., Bockaert J., Grau Y.;

RT "Cloning and functional expression of a Drosophila metabotropic glutamate receptor expressed in the embryonic CNS.";

RL J. Neurosci. 16:6687-6694(1996).

CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.

CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

EMBL: X99675; CAA67993.1; -

GCRDb; GCR_1123;

FlyBase; FBgn0019985; Glu-RA.

InterPro; IPR001828; ANF_receptor.

InterPro; IPR000337; GPCR_Mgr.

Pfam; PF00003; 7tm_3; 1.

Pfam; PF01094; ANF_receptor; 1.

PRINTS; PR00248; GPCRMR.

PRINTS; PR00593; MTABOTROPICR.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.

KW G-protein coupled receptor; transmembrane; Glycoprotein; Signal.

SIGNAL

FT CHAIN 1 25

FT DOMAIN 26 976 METABOTROPIC GLUTAMATE RECEPTOR.

FT TRANSMEM 26 626 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 627 649 I (POTENTIAL).

FT DOMAIN 650 663 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 664 684 II (POTENTIAL).

FT DOMAIN 685 695 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 696 714 III (POTENTIAL).

FT DOMAIN 715 738 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 739 759 IV (POTENTIAL).

FT DOMAIN 760 782 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 783 804 V (POTENTIAL).

FT DOMAIN 805 817 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 818 840 VI (POTENTIAL).

FT DOMAIN 841 850 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 851 876 VII (POTENTIAL).

FT DOMAIN 877 976 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).

Db 357 VFAEFWEENFGCKLGSHGKRNSHIKCTGLERIARDSSYEQ-EGKVQFVIDAVYSMAVA 415
QY 339 IQYVAEKREDDLTDFDYKVDWESV-----FLEALRNTSEFVG-TPVRP-YNNERKANIL 392
Db 416 LH---NMHKDLCPGYIGLCPRMSTIDGKELLYIRAVNFNGSAGTPVTFNENGDAPEGVD 472
QY 393 INOFOL---GOMEKIGYHSHQSHLDLS-----LG 419
Db 473 IFQOITNKSTKEYVIGHWTNO-LHLKVEDMOWAHREHTHPASVCSLCKPCKGERKKTGK 531
QY 420 KPVKW-----VGKTPPKDRT---LIVIEHSQVNPITYIIVSASAS 455
Db 532 VPCWCHCERCBGYNOVDELSCELCPLDORPNMNETGCOLPIIKLEHWSHNAVVPFVA 591
QY 456 VIGVIAATVAFIAFNKYNQRIKMSPHLNNLIIVGCMITYLSIIFLGDLTFLSSVAAP 515
Db 592 ILGIATTFVIVTEVRVNDTPIFVIRASGRELVSLLTGIFLCY-SITFLMI-----AAPD 644
QY 516 PYICTARAWILMAGFSLSGFAMFSTWRVHSIFDTDLKN---KKVIKDYQLFVWVGVLIA 572
Db 645 TIICSRFRVFLGCMCFSYAALLTKNRIHRIFFEQGKKSVTAPKFI SPASQLVITFSLIS 704
QY 573 IDIAIITWQIADP-----FYRETKQLEPLHHEIDDDVIVPENECQSEHMTIFVSIY 627
Db 705 VQLLGVFVFWVDPPHIIIDYGEOTLDP---EKARGVL-----KDISLSLISCL-- 753
QY 628 AYKGLLVFGAFIAWETRHVSIPALNDSKHGIFSIVNYVITCLAGAAISLVLSDRKDLVF 687
Db 754 GYSILLAVTCVYAIKRGVP-ETFEAKPIGFTMYTTCIIWLAFIPIFGFGTAQSAEKMY 812
QY 688 V---LLSFFIIFCTATILCVFVKLVKLKRNPGQVVDKVR-----ATL----- 729
Db 813 IQTTLTVSLSASVSLGMLYMPKVYIIFHPQNVQKRKRFRKAVVTAATMQSKLIQK 872
QY 730 ---RPMKNGNRDSSVCE-LEQLRDVKNT 755
Db 873 GNDRP---NGEVKSELCELTNTSSYKTT 899
RESULT 8
MGR4 RAT
ID MGR4 RAT STANDARD; PRT; 912 AA.
AC P31423;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GPM4 OR GPRCLD OR MGLUR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93332699; PubMed=8338667;
RA O'Hara P.J., Sheppard P.O., Thøgersen H., Venezia D., Haldeman B.A.,
RA McGrane V., Houamed K.M., Thomsen C., Gilbert T.L., Mulvihill E.R.;
RT "The ligand-binding domain in metabotropic glutamate receptors is
RT related to bacterial periplasmic binding proteins.";
RL Neuron 11:41-52(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT

CC EXPRESSION IS SEEN IN THE GRANULE CELLS OF THE CEREBELLUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M92077; ; NOT_ANNOTATED_CDS.
CC EMBL; M90518; AAA93190.1; -;
CC PIR; JH0563; JH0563.
CC GCRDb; GCR_0352; -;
CC GCRDb; GCR_0363; -;
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01054; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS02059; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 912 METABOTROPIC GLUTAMATE RECEPTOR 4.
FT DOMAIN 33 587 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 588 610 I (POTENTIAL).
FT DOMAIN 611 624 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 625 645 II (POTENTIAL).
FT DOMAIN 646 656 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 657 675 III (POTENTIAL).
FT DOMAIN 676 699 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 700 720 IV (POTENTIAL).
FT DOMAIN 721 750 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 751 772 V (POTENTIAL).
FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 786 808 VI (POTENTIAL).
FT DOMAIN 809 821 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 822 847 VII (POTENTIAL).
FT DOMAIN 848 912 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 Q -> R (IN REF. 2).
SQ SEQUENCE 912 AA; 101818 MW; 336430EF19B4B577 CRC64;
Query Match 4.8%; Score 309; DB 1; Length 912;
Best Local Similarity 20.5%; Pred. No. 2.9e-10;
Matches 188; Conservative 148; Mismatches 331; Indels 248; Gaps 40;
QY 30 DVIYIAGFFP-YGDGVNSYTG-----RGV--MPSVKALGHVNEHGKILANYLRHMMWND 81
Db 48 DITLGLGFLPVHGRSGKACGELKKEGHRLEAMFLDRINDPDLPLNITLGLARIL 107
QY 82 TCQNAVGVKSFDDMMH-----SG-----PKNVM-LFGAACHVTVDPIAK 120
Db 108 TCSRDPHAEQLSTFVQALIEKDGTVEVRCGSGPPITTKPERVGVIGASGSSVIMVAN 167
QY 121 ASKHHLTLTOLSVADTHPMETKDAFPNFF-RVVPSENAFNAPRLALKKEFNWTRVGTYYQN 179
Db 168 IURLFKIPQISTAPDLSNDSRYDFSRVPSDTYQQAQMWVDIVRALKWNVSTL-AS 226
QY 180 EPRYSLPNHNHVADLDAMEVEVETQSFVND---VAESLKKLRE----- 220

QY 735 NGRDSSVCELEORLQVKNCRFRKALMEKENELQALIRKL 777
 Db 910 TNNNE-----EERSRLLEKENRELEKTIABKEERVSELHQ 946

RESULT 6

MGR8_RAT
 ID MGR8_RAT STANDARD; PRT; 908 AA.
 AC P70579;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
 GN GRM8 OR GPRC1H OR MGLUR8.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97168760; PubMed=9016353;
 RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
 Westbrook G.L.;
 RT "Cloning and expression of rat metabotropic glutamate receptor 8
 reveals a distinct pharmacological profile."
 RT Mol. Pharmacol. 51:119-125(1997).
 RL -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 ACTIVITY.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
 CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
 CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
 CC HIPPOCAMPUS, CEREBELLUM, AND MAMMARY BODY.
 CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U63288; AB09537.1; -
 CC GCRDB; GCR 1411; -
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgt.
 CC Pfam; PF00003; 7tm_3; 1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC PRINTS; PR00248; GPCRMR.
 CC PRINTS; PR01058; MTABOTROPICR.
 CC PRINTS; PR01058; MTABOTROPICR.
 CC PROSITE; PS00979; G_PROTEIN_REC_F3_1; 1.
 CC PROSITE; PS00980; G_PROTEIN_REC_F3_2; 1.
 CC PROSITE; PS00981; G_PROTEIN_REC_F3_3; 1.
 CC PROSITE; PS0259; G_PROTEIN_REC_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Multigene family; Olfaction.
 KW SIGNAL
 FT CHAIN 1 33 POTENTIAL.
 FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
 FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 608 I (POTENTIAL).
 FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 621 641 II (POTENTIAL).
 FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 648 668 III (POTENTIAL).
 FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 696 716 IV (POTENTIAL).
 FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 747 768 V (POTENTIAL).
 FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 782 803 VI (POTENTIAL).

FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 819 843 VII (POTENTIAL).
 FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 95 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 298 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 452 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 480 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 565 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;
 Query Match 4.9%; Score 316; DB 1; Length 908;
 Best Local Similarity 20.7%; Pred. NO. 1.1e-10;
 Matches 196; Conservative 159; Mismatches 340; Indels 250; Gaps 45;
 QY 4 PSWFPEASLFLLLWSTACGRTRAKR-----SDVYIAGFFP-YGDGVENSVTG--- 49
 Db 12 PCFELLTAKFYWL--TMMQTHSQEYAHVIRVDGDIILGLFPVHAKGERGVPCEGLKK 69
 QY 50 -RGV--MPSVKYLALGHVNEHGKILANYRLHMMNDTCN-----AAGVKSF 93
 Db 70 EKGIRLEAMLYAIDQINKDPDLLSNTTLGVRILDT--CSRDTYALEQSLTFVQALIEKDA 128
 QY 94 FDM-----MHSGPNKM-LFGAACTHVDPIAKSKWHHTQLSYADTHPMFTKDAF 144
 Db 129 SDVKCANGDPPIFTKPKDKISGVICAAASSYIMVANILRLFKIPQISYASTAPELSDNTR 188
 QY 145 PNFF-RVVPSENAFNAFLALLKFNWTRVGYVYQENPRYS-----LPHNMVADLDA 196
 Db 189 YDFSVRPDPSYQAQAMVDIVTALGNVYSTL--ASEGNYGESGVFAFTQISREIGVCV 247
 QY 197 MEVEVYETOSFVNDVAESLKLRE-KDVRILGNFNEHFARKAFCEAYKLDIMGRAYQWL 255
 Db 248 AQSQKIPREPRCGEFEKIKRLETPNARAVIMFANEDDIRRILEAAKLNQSGH-FLWI 306
 QY 256 IMATYTDWNVTDSECSVEEETATALEGAILVDLLPLSTSGD-----ITVAGITAD 307
 Db 307 -----GSDSGMGSKIAPVYQEEIA--EGA--VTILPKRASIDGDFRYRSRTLANNRRN 356
 QY 308 EYLVEY-----DRL-RGTEYSRFHG--YTDYDGIWAALA 338
 Db 357 VVFAEWEENFGCKLGHGKRNHKKCTGLERIANDSSEYQ--EGKVQFVIDAVYSHAYA 415
 QY 339 IQVVAEKR-----EDLTHFDYRVKDWESVFLAELRNTSFEGVTG--PVR 381
 Db 416 LHMHKERCPCGYIGLCPRMWTIDGKELGY-----IRAVNFGSAGTPVT 460
 QY 382 F-YNNERKANILINQFOLGOME---KIGEYHSOKSHLDLS----- 417
 Db 461 FNEGDAPGRYDIFQYQINNKSLEYKIIGHWTNQLHLKVEDMQWANREHTHPASVCSLPC 520
 QY 418 -----LGKPKVW-----VGKTPPKDRT-----LIVIE-H 440
 Db 521 KGERKTKVKGPCPCWHCERCEGYNQVDELSCPLDQRPINRTGQRIPIIKLEWH 580
 QY 441 SQVNPTIYVSASAVIGVIAFVFLAFNFIKYNQRYIKMSSPHLNNLIITVGCMTYLSI 500
 Db 581 S----PWAVVPVFIILGIIATTFVIVTVFYNDTPIVRASGRELVSLLTGIFLCY-SI 635
 QY 501 IFGLDFTTLSSVAAPPYICTARAWILMAGFSLSGAMFSKTRVSHSIFTDLKLN---KKV 557
 Db 636 TELMI-----AAPDTIICSFRIFLGLGCMFSYAALLTKTNRIHRIFEQGGKSVAPKF 689
 QY 558 IKDYQLFMVVGVLADIALIITWQIADP-----FRETQKLEPHENIDDLVIVPENE 612
 Db 690 ISPASQLVITFSLISVQLLGVFVWFVDPPTIIDIYGEQRTLDP---ENARGVL----- 740
 QY 613 YCQSEHMTFVSIYAYKGLLVFGAFIATWETHRSVIPALNDSKHIGFSVYVFTICLAG 672
 Db 741 KDISDLSLCSL--CYSILLMWTCTVYAIKTRGVP-ETFNEAKPIGFTMYTTCIIWLAF 797
 QY 673 AAILSVLSRKDLVFFV---LLSFFIIFCTATLCLVFPKVLKRNPGQVDRKVR--- 726


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Query Match      18.0%; Score 1156.5; DB 1; Length 960;
Best Local Similarity 32.7%; Pred. No. 1:1e-58;
Matches 259; Conservative 167; Mismatches 309; Indels 57; Gaps 16;

QY 18 WST-----ACGR--AKRSDDVYIAGFFPYGDCGVNSYTGKGVNPKVLAHLGHVNEHGKIL 70
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 149 WSTPKPHCOVNRTPSHERRAVYIGALFPMSSGGWPG---GQACQPAVEMAELEDVNSRRDIL 205
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 71 ANYRLHMWNDDQCNAAVGVKSFDDMHSGPNKVMFLGAACTHVTDPDIKASKKHHLTQL 130
   :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:
Db 206 PDYELKLHHDSKCDPGQATKLYELLYNDPIKIILM-PCGSSSVTLVAEARMWNLIIVL 264
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 131 SYADTHP-MFTKDAFPNFRFVPSNAPNAPRALLKKEFNTRVGTIVYQNEPRYSPLPHH 189
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 265 SYGSSSPALSNRQEPFTRTHPSATLHNPTRVKLFKFGWKAKIATIQOTTEVFT----- 319
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 190 MVADLDAME-----VEVETQSFVNDVAESLKLREKDVRIILGNFNEHFAKAFCEA 242
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 320 --SYLDDLEERVKEAGIELTFQSFSDPAVPVKMLKQADRIIVGLFYETEARKEVCEV 377
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 243 YKLDIMYGRAYOWLIMATYSTDMWNTOPS-EGSVEEIIATALEGAILVDLLPLSTSGDITV 301
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 378 YKERLEGGKYVWFLGWADNWFKYDPSINCTVEEMTEAVEGSHITTEIVMLNPANTRSI 437
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 302 AGITADELYVEYDLRGTEYSRFHGY-----TYDGIWAAALAIQYVA-----EKREDL 349
   :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:  :||:
Db 438 SNMTSQEFVEKLTKLKRPHEPTGFGQAPLAYDAIWAIALALNKTSGGGGRSGVRLED- 496
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 350 LTHFDYRVKDNESVLEALNRTSFGVGPVRF-YNNERKANILLNOLFQGWOMEKIGEVH 408
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 497 ---FNINQTTDQIYRAWNSSFEGVSGHVVDASGSRMAWTLIEQLGGGYSKIGIYYD 553
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 409 SOKSHLDLSLGPVKWVGKTPPKDRTLIVIEHSQVNPITYIVSASVIGVITATVFLAF 468
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 554 STKD--DLSWSTDKWIGSSPADQTLVKTFRFLSQKLFISVSVLSGIVLAVVCLSF 611
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 469 NIKYRNQRYIKMSSPHLNLIVGCMITYLSIFIGLDTLSSVAAPFYCTARAWILMA 528
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 612 NIYNSHVRVYIQNSQPNLNLAVGSLAALAAVFLGLDGYHGRSQFPVQCQARLWLLGL 671
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 529 GFSLSFQAMFSKTRVHSHFT---DLKLNKKVKIKYQYLFVWVGVLLADIALIITWQIAD 585
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 672 GFSLGYSMFTKIWMVHVTFVTKKEKKEMWRTLEPMKLYATVGLLVGMDILFALWQIYD 731
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 586 PFYRETKOLEPLHENIDDLVLPENEXYQCSHMTIFVSIYAYKGLLVFGAFLAWETR 645
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 732 PLHRTIETFAKEEPKEDIDVSLPOLEHCSSKMMTWLIGIFYGKGLLLLLGIFLAYETK 791
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 646 HVSIPALNDSKHIGFSVYNVFTITLAGAAISLVLSDRKDLVFLVLSFFIFCTTATLCIV 705
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 792 SVSTEKINDHRAVGMAIYNVAVLCITAPVTWMLSSQDDAAFAFASLAIVFSSYITLVVL 851
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 706 FVPKLVKLRNPGQVVDKVRVATLRPMKNGRRDSSVCELEORLDVKNTRCFRKALME 765
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 852 FVPKMRRL--ITRGWQSEADTMKTGSTNNNE-----EKSRLLEKENELEKEITAE 903
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 766 KENELQALIRKL 777
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 904 KEERVSELRHQL 915
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 4
GBR1_HUMAN
ID GBR1_HUMAN STANDARD; PRT: 961 AA.
AC QUBS5; 095375; 090Q00; 096022; 095975; 095468;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GBL).
GN GABBR1.
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Cerebellum;
RX MEDLINE=99061981; PubMed=9844003;
RA Kaupmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H., Bettler B.,
RA Heid J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
RT expressed and regulate inwardly rectifying K+ channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Brain;
RX Stroop U., Raming K.;
RT "Human mRNA for GABA-B1a receptor.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Fetal brain;
RX MEDLINE=98440782; PubMed=9753614;
RA Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,
RA Zelante L., Gasparini P.;
RT "GABA (gamma-amino-butyric acid) neurotransmission: identification and
RT fine mapping of the human GABAB receptor gene.";
RL Biochem. Biophys. Res. Commun. 250:240-245(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=99014802; PubMed=9798068;
RA Goel V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,
RA Gruen J.R.;
RT "Human gamma-aminobutyric acid B receptor gene: complementary DNA
RT cloning, expression, chromosomal location, and genomic organization.";
RL Biol. Psychiatry 44:659-666(1998).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1C).
RC TISSUE=Cerebellum;
RA Fraser N.J.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
RC TISSUE=Fetal brain;
RX MEDLINE=20184290; PubMed=9933300;
RA Peters H.C., Kaemmer G., Voiz A., Kaupmann K., Ziegler A., Bettler B.,
RA Epplen J.T., Sander T., Rieck O.;
RT "Mapping, genomic structure, and polymorphisms of the human GABAB1
RT receptor gene: evaluation of its involvement in idiopathic
RT generalized epilepsy.";
RL Neurogenetics 2:47-54(1998).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RA Younger R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Cerebellum;
RX MEDLINE=99108069; PubMed=9889352;
RA Makoff A.;
RT "Molecular cloning of human GABAB1 and its tissue distribution.";
RL Brain Res. Mol. Brain Res. 64:137-140(1999).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM 1E).
RC TISSUE=Prostate;
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QY 173 VGTVTQNEPRYSLPHNMVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNE 232
 DB 198 VGTLTQDVORFSEVRNDLTVGLYGEDIESDTSFSDPCTSVKLLKGNVDRIILGQFDQ 257
 QY 233 HFARAFCEAYKIDMGRAYOWILMATYSYDWW- ---NVTQDSECSVEETATALEGAILV 288
 DB 258 NMAAKVCCAYENMTYGSYQWIIIPGWYEPSSWWEQVHTEANSSRCLRNKLLAMEGYIGV 317
 QY 289 DLLPLSTGSDITVAGITADEYLVEYDRLR-GTEYSRFGHYTYDGIWAAALAIQVV- --- 342
 DB 318 DFEPLSSKOIKTISGKTPOQYEREYNNKRSVGPSFHEGYAYDGIWIAKTQLQAMETLH 377
 QY 343 AKREDLLTHEDYRVKDWESVLEALRNSTFEGVTGVPYRNNERKANILINPOLGOME 402
 DB 378 ASSRHQRIQDFNTHTLGRILLNAMNETNFFGVGTGVVFRNGERMGTIKFTQFQDSREV 437
 QY 403 KIGEVHSOKSHLDLSLGGPKVWKGKTPPKDRTLIYIHSOVNPTIYIVSASVIGVIA 462
 DB 438 KYGEYNAVADTLEI-INDTIRFOGSEPPKDKTIIIEQLRKISUPLYSILSALTILGIMA 496
 QY 463 TVELAFNIKYRQYIKMSPHNNLIIVGCMITYLSIIFGLDITLSSVAAFPYICTAR 522
 DB 497 SAFLFENIKNRNOKLIKMSPPYNNLIILGMLSYASIFLGLDGSFVSEKTFETLCTVR 556
 QY 523 AWILMAGFSLSGAMSKTWRVHSIFDTLKLKKVKIDYQLFWMVGVLLAIDIAIITWQ 582
 DB 557 TWILTVGYTFAFCAMFAKTWRVHAIFKNVKKKKIIRKDKLLVIVGGMLLIDILICWQ 616
 QY 583 IADPFYR--ETKOLEPLHNEID- ---DVLVTPENECQSEHMTIFVSIYAYKGLLVF 636
 DB 617 AVDPURRTVEKYSMEP- ---DPAGRDISIRPLLEHCENTHMTIWLGIYAYKGLLMLF 670
 QY 637 GAFLAWETRHSVPALNDSKHGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
 DB 671 GCFLAWETRHSVPALNDSKHGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 730
 QY 697 CTTATLCLVFPKLVKELKPNQGV-DKRVRTLPMKNGRRDSSVCELEQ- ---RLRD 751
 DB 731 CSTITLCLVFPKLVKELKPNQGV-DKRVRTLPMKNGRRDSSVCELEQ- ---RLRD 790
 QY 752 VNTNCRFRKALMEKENLOALRLK- ---GPEARKWIDGVCTGSGNVGSELEPLINDDIV 809
 DB 791 IQSENHRLRMKITELDKDLDEVTMQLDTPKTYIK- ---QNHQELNDTLN- --- 839
 QY 810 RLSAPPVREMPSTTVTMT-SVDSVTSTHVMDNSFVSQSTVMAPSLPPKXKQSTIVE 868
 DB 840 - ---LGNFTSTGCKAILKNHLDQN- ---PQL- ---Q 865
 QY 869 HHSAPAPTMPOIQ-QLQOHLQHQOQOHLQOQOHOQOQOQOQOHHHRLHLEKRN 927
 DB 866 WNTTSPSTCKPDIEDINSPEHIQRLSLQLPIL- ---HHAYLPSIG 908
 QY 928 SVSA 931
 DB 909 GVDA 912

RESULT 2
 GBR2_RAT
 ID GBR2_RAT STANDARD; PRT; 940 AA.
 AC O88871; Q9QWU2; Q9JK36;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
 DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).
 GN GABR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]

SEQUENCE FROM N.A.
 TISSUE=Hypothalamus;
 MEDLINE=99087320; PubMed=9872315;
 Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,
 Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
 Salon J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
 Branchek T.A., Gerald C.;
 "GABA(B) receptors function as a heteromeric assembly of the subunits
 GABA(B)R1 and GABA(B)R2.";
 Nature 396:674-679(1998).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Brain cortex, and Cerebellum;
 MEDLINE=99087322; PubMed=9872317;
 Kaufmann K., Malitschek B., Schuller V., Heid J., Froestl W., Beck P.,
 Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
 Bettler B.;
 "GABA-B receptor subtypes assemble into functional heteromeric
 complexes.";
 Nature 396:683-687(1998).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Brain cortex;
 MEDLINE=20193514; PubMed=10727622;
 Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
 "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
 Brain Res. 860:41-52(2000).
 [4]
 SEQUENCE FROM N.A.
 TISSUE=Hypothalamus;
 Borowsky B., Laz T., Gerald C.;
 Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 [5]
 R1A-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
 TISSUE=Hippocampus;
 MEDLINE=99102694; PubMed=9872744;
 Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 Kornau H.-C.;
 "Role of Heteromer Formation in GABA-B Receptor Function.";
 Science 283:74-77(1999).
 CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 ANTINOCICEPTION.
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 HAPPEN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 PLASMA MEMBRANE.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
 HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
 CEREBELLUM.
 CC -!- DEVELOPMENTAL STAGE: ABUNDANT IN BRAIN CORTEX AND CEREBELLUM
 THROUGHOUT POSTNATAL DEVELOPMENT WHEREAS ITS EXPRESSION IN SPINAL
 CORD GRADUALLY DECREASES.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration

SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.

TISSUE=Brain;

MEDLINE=99263199; PubMed=10328880;

Martin S.C., Russek S.J., Farb D.H.;

"Molecular identification of the human GABABR2: cell surface expression and coupling to adenylyl cyclase in the absence of GABABR1.";

Mol. Cell. Neurosci. 13:180-191(1999).

[7]

RIA-R2 INTERACTION.

MEDLINE=99175124; PubMed=10075644;

Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R., Kargman S., Chateaufeur A., Tsukamoto N., McDonald T., Whiting P., Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F., Bonner T.I., O'Neill G.P.;

"Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.";

J. Biol. Chem. 274:7607-7610(1999).

[8]

RIA-R2 INTERACTION.

MEDLINE=9937752; PubMed=10773016;

Sullivan R., Chateaufeur A., Coulombe N., Kolakowski L.F. Jr., Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K., Abramowitz M., O'Neill G.P., Ng G.Y.K.;

"Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B)) receptors with truncated receptors and metabotropic glutamate receptor 4 supports the GABA(B) heterodimer as the functional receptor.";

J. Pharmacol. Exp. Ther. 293:460-467(2000).

-I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY, STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS, INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND ANTINOCICEPTION.

-I- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO HAPPEN.

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE PLASMA MEMBRANE.

-I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE PRODUCED BY ALTERNATIVE SPLICING.

-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA. WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.

-I- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

-I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. GABA-B RECEPTOR SUBFAMILY.

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EMBL; AJ012188; CA009942.1; -

DR EMBL; AF056085; AAC63228.1; -

DR EMBL; AF095723; AAC63383.1; -

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:04:53 ; Search time 24.07 Seconds
(without alignments)
1858.375 Million cell updates/sec

Title: US-09-715-962-4

Perfect score: 6409

Sequence: 1 MFRSPWPFASLLFLLWST.....SAVGQSCPNIKCDIVEYL 1220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1598	24.9	941	1	GBR2_HUMAN
2	1578.5	24.6	940	1	GBR2_RAT
3	1156.5	18.0	960	1	GBR1_MOUSE
4	1151.5	18.0	961	1	GBR1_HUMAN
5	1134	17.7	991	1	GBR1_RAT
6	316	4.9	908	1	MGR8_RAT
7	312	4.9	908	1	MGR8_HUMAN
8	309	4.8	912	1	MGR4_RAT
9	305	4.8	908	1	MGR8_MOUSE
10	289.5	4.5	912	1	MGR4_HUMAN
11	289.5	4.5	976	1	MGR_DROME
12	286.5	4.5	915	1	MGR7_HUMAN
13	280.5	4.4	915	1	MGR7_RAT
14	278.5	4.3	1212	1	MGR5_HUMAN
15	276.5	4.3	1194	1	MGR1_HUMAN
16	271.5	4.2	1079	1	CASR_MOUSE
17	268	4.2	877	1	MGR6_HUMAN
18	268	4.2	1203	1	MGR5_RAT
19	265.5	4.1	1079	1	CASR_RAT
20	261.5	4.1	1199	1	MGR1_RAT
21	258.5	4.0	871	1	MGR6_RAT
22	256	4.0	1078	1	CASR_HUMAN
23	246	3.8	872	1	MGR2_RAT
24	246	3.8	879	1	MGR3_RAT
25	237.5	3.7	999	1	MGR1_CAEEL
26	231	3.6	877	1	MGR3_HUMAN
27	229	3.6	1085	1	CASR_BOVIN
28	226	3.5	872	1	MGR2_HUMAN
29	211	3.3	550	1	CCF_DROME
30	199.5	3.1	540	1	ANPC_HUMAN
31	196.5	3.1	708	1	GBF_DICDI
32	196	3.1	1231	1	YKT3_CAEEL
33	195	3.0	537	1	ANPC_BOVIN

RESULT 1

ID	GBR2_HUMAN	3.0	1556	1	PRO_DROVI	Q9u6al drosophila
AC	075899; 075974; 075975; Q9UNR1; Q9PIR2;	3.0	635	1	HMLA_DROME	P10105 drosophila
DT	20-AUG-2001 (Rel. 40, Created)	3.0	535	1	ANPC_RAT	P41740 rattus norv
DT	20-AUG-2001 (Rel. 40, Last sequence update)	3.0	758	1	YM38_YEAST	Q03825 saccharomyc
DT	20-AUG-2001 (Rel. 40, Last sequence update)	3.0	536	1	ANPC_MOUSE	P70180 mus musculu
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 (GABABR2) (G PROTEIN-COUPLED RECEPTOR 51) (GPR 51) (HG20).	2.9	885	1	AKA2_MOUSE	O54931 mus musculu
GN	GABBR2 OR GPR51.	2.9	2248	1	CYAL_DROME	P32870 drosophila
OS	Homo sapiens (Human).	2.9	1080	1	HDC_DROME	Q9n2m8 drosophila
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	2.8	1167	1	WC1_NEUCR	Q01371 neuropeptid
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	2.8	514	1	CF23_DROME	Q01522 drosophila
NCBI_TaxID	9606;	2.8	597	1	IXRL_YEAST	P33417 saccharomyc
RP	SEQUENCE FROM N.A. (ISOFORM 2A).	2.8	648	1	KAPC_DICDI	P34099 dictyosteli
RC	TISSUE=Cerebellum;					
RX	MEDLINE=99087321; PubMed=9872316;					
RA	White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H., Barnes A.A., Emson P., Poord S.M., Marshall F.H.;					
RA	"Heterodimerization is required for the formation of a functional GABA(B) receptor."					
RT	Nature 396:679-682(1998).					
RL	[2]					
RN	PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).					
RP	TISSUE=Brain;					
RC	MEDLINE=20193514; PubMed=10727622;					
RX	Clark J.A., Mezey E., Lam A.S., Bonner T.I.;					
RA	"Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";					
RT	Brain Res. 860:41-52(2000).					
RL	[3]					
RN	SEQUENCE FROM N.A. (ISOFORM 2A).					
RP	Liu M., Parker R., McCrear K., Watson J., Baker E., Sutherland G., Herzog H.;					
RA	"Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen.";					
RT	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.					
RL	[4]					
RN	SEQUENCE FROM N.A. (ISOFORM 2A).					
RP	TISSUE=Hippocampus;					
RC	Borowsky B., Laz T., Gerald C.;					
RA	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.					
RL	[5]					
RN	SEQUENCE FROM N.A. (ISOFORM 2A).					
RP	TISSUE=Fetal brain;					
RC	MEDLINE=99189236; PubMed=10087195;					
RX	Ng G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P., Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F., O'Neill G.P., Liu Q.;					
RA	"Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9.";					
RT	Genomics 56:288-295(1999).					
RL	[6]					

ALIGNMENTS

DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 983 AA; 109276 MW; 072F0DBB3A840A80 CRC64;

Query Match	4.4%	Score 281;	DB 11;	Length 983;
Best Local Similarity	20.0%	Pred. No. 1.9e-11;		
Matches 171; Conservative 147; Mismatches 303; Indels 234; Gaps 38;				
QY	30	DVYIAGFP-YGDGVENSYTG-----RGV--MPSVKLALGHVNEHGKIIANRYLRHLMWND	81	
Db	48	DITLGLFPVHGRSGEGKACGELKKEGIHLEAMLFALDRINNDPDLNITILGARILD	107	
QY	82	TQCN-----AAGVKSPFDM-----MHSGPNKM-YLFGAACTHVTDP	119	
Db	108	T-CSDRTHALEQSLTFVRALIEKDGTEVRGSGGPPITIKPERVVGVIAGSGSSVIMVA	166	
QY	120	KASKHHLTQLSYADTHPMETKDAFPNFF-RVVPSENAFNAAPRALALLKEFNWTRVGT	178	
Db	167	NIURLFKIQLSYASTAPDLSNDRYDFSRVPSDLYQAQAMVDIVRALKNYVSTL-A	225	
QY	179	NEPRYSLPHNMVADLDAMEVEVVEVETSFVND---VAESLKKLRE-----	220	
Db	226	SEGSYG-----ESGVEAFIQKRENGGVCIASQSVKIPREPKTGEFDKIIKRLLE	274	
QY	221	-KDVRIILGNFNEHFAKFACEAYKLDIMYGRAYQWLIMATYSTWNVYQDSECSVEE	279	
Db	275	TSNARGIIIFANEDDIRVLEAARRANQTGHFF-WM-----GSDSWGSKSAPVLRLE	328	
QY	280	TALEGAILVDLLPLSTSG-----DITVAGITADEYLVEYDR---LRGTEY	321	
Db	329	---EGAVTILPKRMSVRGFDRYFSRSLDNNRRNIWFAEFMEDNFCHLSRHALKKGSH	385	
QY	322	SRPHG-----VYDGIWAAALAIQVVAEKREDLLTHFY-----	355	
Db	386	KCTNRERRIGQDSAYEGGKVQFVIDAVYANGHALHAM-----HRDLCPRGVGLCP	436	
QY	356	RVKDWESV-FLEALRNFSFEGVTG-PVRF-YNNERKANILINQFOL---GQMERIGEYH	408	
Db	437	RMDPVDGTQLLKYIRNVNFSGIAGNPVTFNENGDPAGRYDIYQYLRNGSAEYKVIG---	493	
QY	409	SQKSHLDLSLGKPKVKNVG-----	426	
Db	494	SWTDHLHLRIER-MQWPGSGQQLPRISCLPCQGERKKTVKGMACCWHECPTGYQYQV	552	
QY	427	-----KT-----PPKDTL---IYIEHSQVNPITYIVSASASVIGVLIATVFLAFN-IK	471	
Db	553	DRYCTKCPYDMRPTENRTSCQPIPIVLEWDSWAVLPLFLAVVG-IAATLFVVVVFVR	611	
QY	472	YRNQRYIKMSSPHLNLIIVGCMITYLSIIFGLDITLSSVAAFPYICTARAWILMAGFS	531	
Db	612	YNDTPIVKASGRELSYLLAGIFLCYATTFMLIAEPDLGT-----CSLRIFLGLGMS	664	
QY	532	LSFGAMFSKTRVHSITFDKLN---KKVIKDYOLFWMVGVLLAIDIAITWQIADPF-	587	
Db	665	ISYAALLTKTNRIYRIFEOGKRVSAPRFISPASOLAITFILLSQLLGICVWFVWDPSH	724	
QY	588	-----YRETKOLEPLHHE-----NIDDLVIVPENECQSEHMTIFVSIYIAYKGLLVGA	638	
Db	725	SVVDFODQRTLDPRFARGVLRKCDISLSLI-----CLLGYSMLLMVFTCT	768	
QY	639	FLAWETRHVSIPALNDSKHIGFSVYNNVFTCLAGAAISLVLSDRKDLVFV---LLSFFII	695	
Db	769	VYAIKTRGVP-ETFNEAKPIGFTMYTCIWLAFIPIFFGTSQSADKLYIQTTTLTVSVS	827	
QY	696	FCTTATLCLVFPVKL 710		
Db	828	LSASVSLGMLYMPKV 842		

[1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed-10731132;
RX Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon K.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bavendine J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J.J., Brokstein P., Brotter I.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablois B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphry L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nilsson K.A., Nixon K., Nusken D.R., Pacleab J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidon-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C.; Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zavari J.S., Zhao M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
DR EMBL; AE003846; AAFF59402.1; -
DR FlyBase; FBgn0019985; Glu-RA.
DR InterPro; IPRO01828; ANF_receptor.
DR InterPro; IPRO00337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 976 AA; 108485 MW; 43A0E1P9I8EDACC4 CRC64;

Query Match 4.5%; Score 285.5; DB 5; Length 976;
Best Local Similarity 19.2%; Pred. No. 8.9e-12;
Matches 171; Conservative 130; Mismatches 345; Indels 245; Gaps 31;

QY 30 DVYIAGFPFGDGVSNTYG-----RGV--MPSVKALGLGHVNEHGKILANYLRHMWNNDT 82
Db :|::||::||::||::||::||::||::||::||::||::||:
44 DIILGGLFPVHEKGAPCGPKVNRGVQRLEAMLYADRVNNDPNILPGITIGVHILD 103
QY :|::||::||::||::||::||::||::||::||::||:
83 QCNAAVGVKSFFDDMMHSKPVMFLGAACHTVTD----- 117
Db :|::||::||::||::||::||::||::||::||::||:
104 CSRDITYALNQSLQSFVRASLNLDTSYGECADGGSPQLRKNASSGPVFVGIGGSYSVLSIQ 163
QY :|::||::||::||::||::||::||::||::||::||:
118 IAKASHKHLLTLQSAYDT-HPMFTKDAPPNFRRVPSENAFNAPRALALKKFNNTRVGT 176
Db :|::||::||::||::||::||::||::||::||::||:
164 VANLLRLFHPDQVSPASTAKTSLDKTFDLDFARVPPDFFOSVALVDLVKDNFWSTVI 223
QY :|::||::||::||::||::||::||::||::||::||:
177 YQ--NEPRYSLPHNHMVADLDANEVEVVE-----TQSFVNDAESLK-----L 218

Query Match	4.5%;	Score	285.5;	DB	5;	Length	976;
Best Local Similarity	19.2%;	Pred. No.	8.9e-12;				
Matches	171;	Conservative	130;	Mismatches	345;	Indels	245;
Gaps	31;						
QY	30	DVTIAGFFPYGDGVNSYTG	-----RCV--MPSVKKALGHVNEHGKILANLYRLHMMNDT	82			
		I : : I I I :	I I I : : : I I I :				
Db	44	DIILGLFPVHEKGEAPCGPKVYNRGVQRLEAMLYAIDRVNNDPNILPGITGVHILDT	103				
		I : : I I I :	I I I : : : I I I :				
QY	83	QCNAAVGVKSFFDMHSGPNKVMFLFGAACTHTVDP	-----	117			
		: : : I I I :	I I I : : : I I I :				
Db	104	CSRDYVALNQSLOFVRASLNNLDTSGYECADGGSPQLRKNASGPGVFGVIGGSYSVSQ	163				
		I : : I I I :	I I I : : : I I I :				
QY	118	IAKASHHHIITOLSYADT-HPMTKDAFPNFRVVPSENAFNAPLALLKEFNTRVCTV	176				
		I : : I I I : I I I :	I I I : I I I : I I I :				
Db	164	VANLLRUFHLPQSVSPASTAKTLDSDKTRFDLFARTVPPDPTQSFVALVDILDKNFNYSYSTI	223				
		I : : I I I :	I I I : I I I : I I I :				
QY	177	YQ--NEPRYGLPHNHIMVADLDAMEVEVVE-----TQSEFVNDAESLKK-----L	218				
		I : : I I I :	I I I : I I I : I I I :				


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Db 811 SVLSATVALGCMFVPKVYIILAKP-----ERNVRSATFTTVRMHVGDGKSSSAASRSS 866
QY 741 SVCELEQRLDVKNTRCFR--KALMEKENELQALIRK--LGPEAR-----KWID 786
Db 867 SLVNLWKR--RGSSGETLRYKGRRLAPHKSEIECTFPKSGMNGGRATWTSSNGKSVSNAQ 925
QY 787 GVTCTGGSNGVSELEPILNDDIVLSAPVPRREMPSTTVTMTSVDSTVTHVMDNSFV 846
Db 926 NEKSSRGHLWRLSIHIN-----KKENPNQTA-----954
QY 847 SVQSTVMAPSLPKKKKQSIVEHHSHAP-----TMMQPIQOOLQOHOQOHOQOHLQ 902
Db 955 -----IKPFSKSTSSRRHSSSATPETSATKLYDVSEAEQYPAQVRPQTPSPIS 1004
QY 903 QOQHQQOQOQOQOHHHLEKRNVSQAOTDDNIGSTITAGKRSAGGDCSSMRERROST 962
Db 1005 TVSH-----RTASVSRTEDDAPTQSEPPQPPRSSSQSLMEQISV 1045
QY 963 ASRHYDGSQPTTARPKYSSHRNSSTNISTQSLSNMCHSKPSTPAVTKTPTASDHR 1022
Db 1046 VTRF-----TANI-----SELNSM-----MLSTATPG--- 1067
QY 1023 RTSGSALKSNFVVSQSLDWTHTLSHAKORSPR---NYASPORCAEHGCG--HGMTYD 1077
Db 1068 -TWATPLCSSYLPRIEIQLTPTMTTFAEIQPLPSIEVNGASQSARKOSNGSVKEGTAPT 1126
QY 1078 PNTTSPIQRSYSEKRNKRHPKQKGTVCQSETDSE 1113
Db 1127 PSAQDLLEELVALPPSPFRSDISGSASPSPVSE 1162

RESULT 12
Q98UC4
ID Q98UC4 PRELIMINARY; PRT; 1242 AA.
AC Q98UC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICED VARIANT F.
GN MGLUR5F.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA StorzJohann L.L., Stormann T.M., Parks T.N.;
RT "Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227203; AAK01488.1;
KW Receptor.
SQ SEQUENCE 1242 AA; 138063 MW; 9ED84AFEFA2CF0EB CRC64;
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Query Match 4.78; Score 303; DB 13; Length 1242;
Best Local Similarity 18.98; Pred. No. 7e-13;
Matches 260; Conservative 204; Mismatches 471; Indels 442; Gaps 61;

QY 12 LLFLLWSTACGR-----TAKR-----SDVYIAGFF-----PYGDGVENSYTCR- 50
Db 7 LAILLLEDVCGNGLLVSAQANERRVVAHMPGDIIGALFSVHHQPIVDKVRHKCGEV 66
QY 51 ---GV---MPSVKALGHVNEHGKILANYRLHMMWMDTQCNAAGVKGSFFDMM----- 97
Db 67 REQYGIQVRVEMALTLDRINLDPILLNPITLGCETRDSCWHSVALEQSIEFIRDSLSS 126
QY 98 -----HSGPNKVMLFCACTHVDPTAKAKSHWHLFQLSYADTH-PMF 139
Db 127 EEERGVRVCDGSSSFHSKPIVGIVGPGSSVAIQVONLLQLFNIPQIAYSATSMDS 186
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QY 140 TKDAPPNFRFVVPSENAFNAPRLALLKERNWTRVGTYYONEPRYSLPHNHMWADLDAME- 198
Db 187 DKTLEKYMFRVVPDQAQARAMVDIVKRYNWTYVSAVH--TEGNYGSGMEAFKDMAKEG 245
QY 199 VEVVETQSFVNDVAES-----LKKLRE--KDVRIILGNFNEHFARKAFCAYKLDYMGRA 251
Db 246 ICIAHSYKIKYSNAGEOSFKLLKRLKSLHPKARVV-----ACFCE-----GMT 288
QY 252 YQWLIMATYSTDWNVNTQDSECSVEIATALEGAILLDLLPLSTSG-----DIT----- 300
Db 289 VRGLLMA-----MRLGLAGE-----FLLCSGDWADRYDVTGYQRE 326
QY 301 -VAGITA-----DEYLVEYD-----RLRG--TEYSRF-- 325
Db 327 AVGGITIKLQSPDKWFDYDYLRLPETNHRNPWFQEFQWHRFOCRLEGFPQENPKYNT 386
QY 326 -----GTYDGIWAALAIQ-----YVAEKREDLLTHFDYRKVD 359
Db 387 CTSQMTLRTQHVQDSKMGFVINAIYSMAYGLHNMQLSLCPGYVG--LCDAMKPIDGR--- 441
QY 360 WESVFLEALRNTSFEGVTGVPVFRYNNERKANLILINOFOLGQMEKIG----- 405
Db 442 ---KLESLMKNTFTGSGDMILFDENGSP---GRYEIMNFKMKGKDYFDYINVSWDN 495
QY 406 -----EYHSQSHLDLSL-GKP-----VKWVGK-----TPPKDRTLIYIEHS- 441
Db 496 GELKMDDEIWESEKNIIIRSCVCEPKGQIKVIRKGEVSCCWTCTPCKENEYVDFEYTC 555
QY 442 -----QVNPITYIVSASASVIGVII-----ATVFL-AFNIKYRNQRY 477
Db 556 KACQLGSPNDELTCGDLIPVQVLRMGDPEIAAVVACGLGLATLFTVFAIFIMYRDTVP 615
QY 478 IKMSSPHLNLNLIIVG-----CMIT-----YLSIFLGLDFTLSSVAAPFYICTA 521
Db 616 VKSSRELICYIILAGICLGLCTFCLIAKPOQIYCYLQIRIGLSP----- 661
QY 522 RAWILMAGSLSFGAMFSKTRVHSIFTDLKLNKKVIKDYQLFM-----VVGVLALID 574
Db 662 -----AMSYALVTKTNRARIAGSK--KKICTKKPRFMSACAQVIAFILICIQ 710
QY 575 IAIITWQIADPYRETQKLEPLH--HENTDDVLVLPENECYSEHMTIFVSIYAYKGLL 633
Db 711 LGIIVALEFTMEP-----PDIMHDYPSIREVYLI-----CNTNLGVVYTP--GYNGLL 756
QY 634 LVFGAFLAWETRHSVIPA--LNDKSHIGFSVYNVFTCLAGAAISLVLSRDKDLVFLVLSF 692
Db 757 ILSCIFYAFKTRNV--PANFNEAKYIATFTYTCIIWLAFVPIYF-----GSNYKIITMCF 810
QY 693 FTIFCTTATCLVFPVKLVELKRNPGQVVDKVRATLR-----PMKNGRRDS 740
Db 811 SVLSATVALGCMFVPKVYIILAKP---ERNVRSATFTTVRMHVGDGKSSSAASRSS 866
QY 741 SVCELEQRLDVKNTRCFR--KALMEKENELQALIRKLGPEARKWIDGVTCTGGSNVGSE 799
Db 867 SLVNLWKR--RGSSGETLRYKGRRLAPHKSEIECTFPK-----GSMNGGRATMTS 915
QY 800 LEPILLNDDIVLSAPVPRREMPSTTVTMTSVDSTVTHVMDNSFVSQSTVMAPSLPP 859
Db 916 EESVCIPECNRSRSESRDEKEVP-----VKDALTG----- 945
QY 860 KKKKOSIVBHHSHAPAPTMQPIQOOLQOHOQOHOQOHOQOHOQOHOQOHOQOHOQH 919
Db 946 -KKTGNCV-----SLIVPQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 993
QY 920 HRHLEKRN-----VSAQTDNIGSITAGKRSGG-----DCSSMRER----- 958
Db 994 STHINKENPNQTAIVKPKSPKSTDSRRHSSATFPETSATKLYDVSEAEQYPAQVRPQT 1053
QY 959 -----RQSTASRHYDGSQPTTARPKYSSHRNS-----STNISTQSLSNM 1001
Db 1054 PSPISVSHRTASVSRTEDDAPTQSEPPQPPRSSSQSLMEQISVYVTRFTANISELSNM 1113
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QY 694 IIFCTTATCLVFPVKLVKELKRNPGQVWVKVRATLRPMKNG-----RRDSS-----V 742
Db 392 FLIGTTMILGLVFPVRWGLYQDPQG-----DNKISNSHSHGVPRRDSAYSPDAEI 444
QY 743 CELEQRLDVK 753
Db 445 RRLKQRISELE 455

RESULT 10
Q90Y85 PRELIMINARY; PRT; 153 AA.
AC Q90Y85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GABA-B RECEPTOR 2 (FRAGMENT).
GN GABABR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface of
expression and coupling to adenylyl cyclase in the absence of
GABABR1.";
RT Mol. Cell. Neurosci. 13:180-191(1999).
RL EMBL; AF112975; AAF18937.1;
KW Receptor.
FT NON_TER 1
FT NON_TER 153
FT SEQUENCE 153 AA; 17211 MW; 43354B7AAF123D6C CRC64;

Query Match 5.1%; Score 329.5; DB 11; Length 153;
Best Local Similarity 41.2%; Pred. No. 3.le-16;
Matches 63; Conservative 37; Mismatches 52; Indels 1; Gaps 1;
QY 384 NERKANILINPOLGOMEKIGYHQSOKSHLDLSLGPVKVWGKTPKDRTLIYIEHSQV 443
Db 2 NGERMGTIKFTQDSREKVGEYNAVADTLEI-INDTIRFQSGEPKDKTIIIEQLRKI 60
QY 444 NPTIYIVSASVIGVLIATVFLAFNKKYRNQYIKMSSPHLNLIIVGCMITVLSIFL 503
Db 61 SLPLYLSALTILGIMIMASAFNFNKNRQKLIKMSPPYMNLIILGGLMSYASIFLF 120
QY 504 GLDTTLLSSVAAFPYICTARAWILMAGFSLSFGA 536
Db 121 GLDGSFVSEKTFETCTVTRWILTVGYTAFGA 153

RESULT 11
Q98UC5 PRELIMINARY; PRT; 1188 AA.
AC Q98UC5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICE VARIANT B.
GN MGLUR5B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Storjohann L.L., Stormann T.M., Parks T.N.;

RT "Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
KW EMBL; AF227202; AAK01487.1;
SQ SEQUENCE 1188 AA; 132053 MW; 6C179BF8C8045BBD CRC64;

Query Match 4.7%; Score 304; DB 13; Length 1188;
Best Local Similarity 18.4%; Pred. No. 5.5e-13;
Matches 250; Conservative 199; Mismatches 453; Indels 454; Gaps 60;
QY 12 LFLILLWSTACGR-----TAKR-----SDVIAGFF-----PYGDGVENSYTGR- 50
Db 7 LAIILLKEDVCGNFGLLVSAQANERRVVAHPGDIIGALFSVHHQPTVDKVKHERKCEV 66
QY 51 ---GV---MPSVKLALGHVNEHGKILANRLHMMWNTQCNAAVGVKSFDDMM----- 97
Db 67 REQYGIQVREALHTLDRLNDPTLLPNITLGCETRDSCHWSVALEQSIETIRDSLSS 126
QY 98 -----HSGPNKVMFGAACTHTVDTAKAKSHWLQLSVADTH-PMF 139
Db 127 EEEEGVRCVDGSSSFHSKXPIVGVIGSGSSVAIQVONLLQFNIPQIAYSATSMDS 186
QY 140 TKDAPPNFFRVVPSENAFNAPRLALLKEFNMTVGTVYQNEPRYSLPHNHMVADLDAME- 198
Db 187 DKTLLFKYPMRVVPSDAQARAWDIVKRYNMTYVSAVH-TEGNYGESGWEAFKDMAKEG 245
QY 199 VEVVETQSFVNDVAES-----LKKLRE--KDVRIILGNFNEHFARKACEAYKLDMYGRA 251
Db 246 ICIAHSYKIYSNAGEQSFDKLLRLKRLSHLPKRVV-----ACFCE-----GMT 288
QY 252 YQWLIMATYSTDWNVTQDSECSVEEATALEGATLVLLPLSTSG-----DIT----- 300
Db 289 VRGLLMA-----MRRGLAGE-----FLLGSDGWDADRYDVTGYORE 326
QY 301 -VAGITA-----DEYLVEYD-----RLRG--TEYSRFH-- 325
Db 327 AVGGITIKLQSPDKVWFDDYVLELRPETNHRNPWFQEFWQHRFOCRLEGGFOENPKYNT 386
QY 326 -----GYTDGTWAAALATQ-----YVAEKREDLLTHFYRVKD 359
Db 387 CTSQMTLRTQHVQDSKMGFVINAISYMAVGLHNMQLSLCPGVG--LCDAMKPIDGR--- 441
QY 360 WESVFLRALRNTPEGVTPGVFRVYNNERKANILINQFOLGOMEKIG----- 405
Db 442 ---KLLESMTNTFTGVSQDMLFDENGDSF---GRYEIMNFKKMGKDYFYINVGSWDN 495
QY 406 -----EYHSOKSHLDLSL-GKP-----VKWVGK-----TPPKDRTLIYIEHS- 441
Db 496 GELKMDDEIWSEKNNIIRSCPECKEQIKVIRKGEVSCCWTCTPCKENEYVFDEYTC 555
QY 442 -----QVNPTIYIVSASVIGVII-----ATVFL-AFNIKRYNORY 477
Db 556 KACQLGSPNDELTCGLIPVQYLRWGDPEPIAAVWVFAFLGLLATLFTVTAIFMTRDPV 615
QY 478 IKMSSPHLNLIIVG-----CMIT-----YLSIIFGLDITLSSVAAFPYICTA 521
Db 616 VKSSRELCTIILGICIGYLCCTFCLIAKPOQIYCYLQIRIGLSP----- 661
QY 522 RAWILMAGFSLSFAMFSKTRWRVHSIFTDLKNKVKIKDYQLFM-----VVGVLALD 574
Db 662 -----AMYSALVTKTNRARIARLAGSK--KKICTKPKPFMSACAQLVIAFILICIQ 710
QY 575 IAITTWIADFFYRETKOLEPLH--HENIDDLVLTIPENEYCOSEHMTIFVSIYAYKGL 633
Db 711 LGIIVALTIMEP-----PDMHDPSPSIREVYLI-----CNTTNLGVVTPV--GYNGL 756
QY 634 LVFGAFLAWETRHVSIPA-LNDSKHIGFSVYNVFTCLAGAAISLVLSDRKDLVFLVLSF 692
Db 757 ILSCTFYAFKTRNV--PANFNEAKYIAFTMTCTCIWLAFAVFIYF-----GSNYKITMCF 810
QY 693 FIIFCTTATCLVFPVKLVKELKRNPGQVWVKVRATLR-----PSKNGRRDS 740

D	b		330	TVEDLENRCMEAGVEIVTRQSFSDPTDAVRNLRQDDARIIVGLFFVVAARRVLCBMYKQ	389
Q	y		246	DMYGRAYOWLIMATYSTDWNVNVTQDSE--CSVEEITATALEGAILVDLLPLSTSGSDITVA	302
D	b		390	QLXGRAHWFFIGWYEDNNYEVLNKAEGITCTVEQMRIAAEGHLITEALMWNONNOTTIS	449
Q	y		303	GITADEX--LVEXDRLR-----GTEYSRF-HGY-----TYD	330
D	b		450	GMTABEFRLVLLYPULAKFLLOCAFFLRHRHNOALIEBGYDINHRYDEPGYQEAPLAYD	509
Q	y		331	GIWAALAIOYYAEK--REDLLTHFDYRVKDWEVSFLEALRNTSPFGTVGPVRFYN-NE	386
D	b		510	AVMSVALAFNMKTMERLTGKGSLRDFTYTDKEIADIEAYAMNSTOFLGVSGVVAFSSQGD	569
Q	y		387	RKANILINOFOLGOMEKIGEYHSOKSHLDLSLGPKVKWG-----	426
D	b		570	RIALTOIEOMIDGKYELGYDTOLD--NLWLNTIEWIGGGKKTKHVTTPEPNKNGPSKD	627
Q	y		427	-----KTTPK-----	431
D	b		628	DVNRGSUTSLSEKNDSEKNPSSASLOQAQPAVPKPKKLISDAGKDTVTKVKNENEP	687
Q	y		432	-----	431
D	b		688	GFSKOFEKESIGVANRRNSSATKKENEKILLVKTVPKSLIKESDNENVPSRRTKSQPVG	747
Q	y		432	-----	431
D	b		748	KKVYESSTRVRREFDSFDRREKYLSDMIDYDRSDEDVEPKLSWEPDLTLRRRFSVNE	807
Q	y		432	-----	431
D	b		808	YHSSLEGEERIDLVSGSTMRGSVRMPQNAEDERPVI LAETINNKLKELKEQRESTN	867
Q	y		432	-----DRTLIIYEHGOVNTI-----YIVSAS-----ASV--IGVIIATVFILA	467
D	b		868	VFRNRRDDKTIDEVKGSKITGTSKOHVEEVKYNETASNEDDDDNAQVKHGHTITKIFSIA	927
Q	y		468	FNIK-----	471
D	b		928	QRMKEKSKSEEDENDKENDKVKKDENKDEQKLPPEPELEAKKAWTFPIAETS PD	987
Q	y		472	-----YRNORY-----	477
D	b		988	IPGENOILQEYQVKIGKRNRKYRCIGINTDISRSKSIKTFISKSGADDLVVYHDGRLR	1047
Q	y		478	-----	477
D	b		1048	DIGOTTENLKNORKNHKHTEPDIPVDIGHSDRDRVREIGVNTKLPKIIPP IAEHMVH	1107
Q	y		478	-----IKMSSPHANLII-----	490
D	b		1108	KNGKURDIGTSTDKFPWPIDDGTDIYMHPITDRKKLANKLIVPPDPDNGPYKMPTKEDR	1167
Q	y		491	----VGCMIITY-----LSIIFLGIDTTLSSVAAF	515
D	b		1168	RTYYKCEVHFPGTEWRRLFNKIHGKYKLRPSHHWLYTLVFSVLYI-LFVFI FSNMF	1226
Q	y		516	PVI-----	518
D	b		1227	DFIKDDASKRVPIMKMAOPFISFTPIGRTPNKAVSFDP RNSTEVMKEYAGIMALLEKYG	1286
Q	y		519	-----CTARAWI-----LMAGF-----SLSFGAM	537
D	b		1287	DYGHNPFGTCTANEKF GYPSGPCVFLKVNRIIGFKTEPYNSDEL V KAKIDEVEFTAL	1346
Q	y		538	-----FSKTW-----RVHSIFTD-----	550
D	b		1347	KRLLENTYTEEGLHNRWTICRSDDKNVLI EFHP E PAIRTEYTDIEEK IEYIANEGKKS	1406
Q	y		551	-----LKL NKK-----VIKDYOLF MVV-----GVLLA ID	574
D	b		1407	FEGPNDVNRIVALKINKLNKANERVHINC KIVIOSHPVCNTMLFCVVICLSVILGID	1466

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Qy 575 IAITWTNQ---IADPF--YRETKOLE-PLUHNENIDDLVIPNEVCQSEHMTIFVSIYA 628
      ::      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1467 GRFVSPEEYPKIDPLQRVLTEPLEDDPV--STTDDIKIRPELEHCESORNMMGLVIYG 1524
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 629 YKGLLVFGAFLAWETRHYSIPALNDSKHGFSVTNVFTTCCLAGAAISILVLSDRKDLVFV 688
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1525 FKGLILVFGFLAYETSFKVKQINDSRVGSINVVVLCITAPVGWVITASODASFA 1584
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 689 LLSFFLIIFTATLCLVFPVKLVELKRNPOGVVDKRVKVRATLRPMSKNRDSSVC-ELEQ 747
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1585 FVALAVIFCCFLSMLLTFVPKVIEVTRHPKRAESKYNP-----DSAISKDEEE 1633
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 748 RLRDVKNTRCFRKALMEKENEQALIRLK---GPEARWKIDGVTTCTGGSNVNGSELEP 802
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1634 RYQLVTENEELQRLTIQKEEKIRVRLQRILVERGDAKGTGLNGATGVASAAVATTSPQ 1691
      :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT    9
Og6954     PRELIMINARY;   PRT;   528 AA..
AC          O96954;
DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE GABA-LIKE RECEPTOR.
GN MGRL.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
ON [1]
RR SEQUENCE FROM N.A.
RA Perovic S., Prokic I., Krasko A., Mueller I.M., Mueller W.E.G.;
RT "Origin of neuronal receptors in Metazoa: cloning of a metabotropic
RT glutamate-like receptor from the marine sponge Geodia cydonium.";
EL Cell Tissue Res. 0;0-0(0).
DR EMBL; Y17211; CAA76688.1; -.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE      528 AA;  58641 MW;  0B99DD8357FEAB3B1 CRC64;
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3

GN Y41G9A.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Ryan E., Wohlman P., Walker C., Fielder T.;
RT "The sequence of C. elegans cosmid Y41G9A."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006761; AAF60549.1; --
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 816 AA; 92251 MW; 4363D11A46CECAL CRC64;
Query Match 13.4%; Score 856.5; DB 5; Length 816;
Best Local Similarity 28.3%; Pred. No. 3.1e-53;
Matches 221; Conservative 164; Mismatches 327; Indels 69; Gaps 22;
QY 49 GRGVMSYKIALGHVNEHGHKILANYRLHMWNDRQNAAGVGVKFFDMHSGPNKVMFLG 108
DB 11 GEACLPAVENALADVNSRLDLPGYVLNMTNHNSSQCPGLAMQOLYDFLYKPTKMLL- 69
QY 109 AACTHTDPTAKSKWHLTQLSYADTHP-METKDAFPNFRVVPSENAFNAPRLALIKE 167
DB 70 TGCSPVTVIAEAPWVKLVLSGGSPALSNRNPFTLTPSPANMQNPTRIHIMEK 129
QY 168 FNRVTGVYQNEPRYSLPHNHMVADLDAMEVE---VVETQSFNDVAESLKLREKQVR 224
DB 130 FKWKRTILMSVEEVFT---TAKDLEATARKGKIKVDRQSFYCDPTDANKTLQRQDAR 185
QY 225 IILGNFNEHFAKAFCAEYKLDYGRAYQWLIMATYSTDMNVTQDSE---CSVEEITATA 281
DB 186 IIVGLEFVTEARKVLCQAYHGLYGRYVWFIFGWYA-DTWYIPPEEHLNCTAEQWTEA 244
QY 282 LEGAILVDLLPLSTGSDITVAGITADELYVEYDLRGTEY-----SRPHGY-----TYDG 331
DB 245 AEYHFTTESVMSLRNDTPALSEMTGMF-----QQRUTQYFQKDTANVGGEPEAPLAYDA 299
QY 332 IWAALAIQYVAEKREDLLTH-----FDYRVKDWESVFEALRNTSEFEGVGPVRFYNN- 385
DB 300 VWALAFNCT---RNNLPSHIRLENYTDYDKVTLADTLFQCVKNTSPRGVSGKVMFSDSG 356
QY 386 ERKANILNQFQGMKEIGEYHSQKSHLDLSGKPKVWV-GKTPPKDRTLIIYIEHSQVN 444
DB 357 DRIARTQIEQMOGKGYKIMGYDTSG--DLEWYNKEQWLNGKGPDPSTVKKHMTVS 414
QY 445 PTIYIVSASASVIGVIATVFLAFNINQRYIKMSSPHNLIIIGCMITLISIFLG 504
DB 415 NEFYPTILFAVLGIAACVFIYLFQKHHERLIIIFQSOECNNILLEGCSLCSLSFLG 474
QY 505 L--DTTLLSSVAAPFYICTARWILMAGFSLSGFAMFSKTRWRVHSIFTD-----LKLKK 556
DB 475 LPSDDISISESLFPLLCARVITLLFGFTFYAGSMFAKVIWVRHGATENQOLASRKDE 534

557 VIKDYQLFMVGVGLLAIDIAITITWQIADPFYRETKQLEPLH--HENIDDLVLPENYXC 614
DB 535 PISSKFFYIVAAALRAVDVFCVFWVLIDPLHL-TSQKPLFTPADSEDEIMPVLQOC 593
QY 615 QSEHMTIFVSIYAYKGLLLVFGAFLAWETRVSPALNDSKHIGFSVYNVFI-TCLAGA 673
DB 594 QSNQOEVGWIGIIMGPKLLLVFGTFLSYETRLKLRFINDSRFVGLAIYNVAVMTLVTP 653
QY 674 AISLVLSDRKGLVFLVLLSFFIIFCTTATLCLVFVKLVKLRNPKQGVVDKRVATLRP-- 731
DB 654 VVTLLIHGKVDANFAFISL-----TVGLIYGPKIRHIIKIVPPSADEIQLNGNVGPGV 705
QY 732 MSKNG-----ROSSVCELEQRLRDVKNTCNCRPKALMEKENELQALIRKLGPEARKW 784
DB 706 MSKVDQKRYDMLKKNETLQIOIEKERKIHECKERLEELTKNSETEDMNAQLLCENDKO 765
QY 785 I 785
DB 766 I 766

RESULT 7
Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE COSMID ZK180.
GN ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Pauley A., Le T.T.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; --
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00003; 7tm_3; 1.
DR PROSITE; PS0225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 10.1%; Score 646.5; DB 5; Length 402;
Best Local Similarity 35.1%; Pred. No. 1.6e-38;
Matches 149; Conservative 68; Mismatches 114; Indels 93; Gaps 11;

Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
*The genome sequence of *Drosophila melanogaster*.
Science 287:2185-2195(2000).
DR EMBL: AE003588; AAF51465.2; -
DR FlyBase: FBgn0031275; GABA-B-R3.
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR000005; HTHArac.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PROSITE: PS0259; G_PROTEIN_REC_P3_4; 1.
DR PROSITE: PS00044; HTH_ARAC_FAMILY_1; UNKNOWN_1.
SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRO 6C4;

Query Match 19.2% Score 1229; DB 5; Length 1305;
Best Local Similarity 30.5%; Pred. No. 7.1e-80;
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps 34;

QY 48 TGRGVP-----SVKALGHVNHGKILANYLRHMMWMDTQNAAYGVKSFDDMMHSG 100
DB 163 TSGRPDPGLSELGAATMAVEHINRK-RLLPGYTLELVNTDQDPCGVGDVFHAIYQ 221
QY 101 PN--KVMFLFGAACHTVTDPTAKASKHWHLTQLSYADTHPMET-KDAPNFRVVPSENAF 157
DB 222 PSTRMVLLGSACSEVTESLAKVVPYVNIQVSGFSPALSDRREFPYFYRTVAPDSSH 281
QY 158 NAPRLALKKFNFRVGTGVYQNEPRYSLPNHHMYADLDAMEVVEVYEQSF-VNDVAESLK 216
DB 282 NPARIATIRKFGWGTVTTFSONEEVHSLAVNNLVTELEAANISCAAYITFAATDFKEOLL 341
QY 217 KLREKDVRIILGNFNEHFARFACFEAYKLDYGRAYQWLIMATYSTDMVNTQDSECSVE 276
DB 342 LLRETDTRIIGSFQELAPOILCEAYRLRMFGADYAWILHESMGAPWW-PDQRTACSNH 400
QY 277 EIATALSGAILVDLLPLSTSGDIIVAGITADEYLVEYDLRGTEYSRPHG----- 326
DB 401 ELQAVENLIIVVSTHNSIVGNVNSYGLNNHMF---NSQLR-KQSAQFHGDGFGSGYGS 456
QY 327 -----YTDGIGWAAALAIQYVAE----- 344
DB 457 RISTAAQTQSDRRRRRGVGTSGHGLFPEALISOYAPQTYDAVWALALALRAEEHWRPN 516
QY 345 KREDLLTHEDYRVKD--WESVFLBALNRTSPGVTPGVYRNNERKANILNQFQLOME 402
DB 517 EQSKLOGDFYTRSDMAWE--FLOOMGKLHPLGVSGPVSFSGPDRVGTTFAYQIQRLGLE 574
QY 403 KIGEVHSOKSHLDLSLG--KPVKWGKTPPKDRTLIYEHSOVNPTIYVSASASVIGVI 460
DB 575 PVALLYPATDALDPCRPVKKVHSGOVPIAKRVFLRVATLAPLAFYTATLSSVGIA 634
QY 461 IATVFLAFNIKYRNQRIKMSPHNLNLIIVGCMITVLSIIFLGLD--TTLSSVAAFPYI 518
DB 635 LAIAFLAFLNHFRLKALKLSSPKLSNITAGVCIFVATVILLGLDHSFLPSAEDSFATV 694
QY 519 CTARAWILMAGFSLSPGAMFSKTWRVHSIP--TDLKLNKKVIKQYQFLPMVGVVLLADIA 576
DB 695 CTARVYLLSAGFSLAFSGMFAKTYVRHRIEFTRTGSVFKDKMLQIDQLILLVGLLLVDAL 754
QY 577 IITWQIADPPYRETKOLEPLHLENID-----DVLVIPENECQSEHMTLFVSIIVAYK 630
DB 755 LVTUWVYDPMERH-----LHNLTLELSATDRSVYTPQVQVECRSQHTQWLSVLYAYK 808
QY 631 GLLLVGFAFLAWETRHYSPALNDSKHIGFSGVNVVFTCLAGAAISLVLSDRKDLVFLVL 690
DB 809 GLLLVGVYMAWETRHVKIPALNDSQYIGVSVSVYITSAIVVYVLANLISERVTLAFITI 868
QY 691 SFFTICTATCLVFPVKLVEL--KRNPQGVVDKRVKRVATLRPMKNGRR-----DSSVCEL 745
DB 869 TALLTSTATPCLCLFIPKLIKDIARN--DIIDPVIHSMGLKMCNTRFRVVDOR--EL 924

Qy	746	BQRLRDVKNTNCRFKALMEKENELQA---	-TRKLGPEARKWIDGVTCTGGSNV-----G	797
Dt	746	---: : : ---RVIK-----KEIQALDAEIRKLERLESGLTFTSTPTSSSLLTGG	974	
Db	925	QYRY-EVON---	RVIK-----KEIQALDAEIRKLERLESGLTFTSTPTSSSLLTGG	974
Qy	798	SELEPIILNDDIVRLSAPPVRREMPSTTVTEM	SVDTSVTSHVMDN---SPFVSQSVTWMA	854
Db	975	GHLAP-	-----ELVTSGISOTPAASKNRTPSISGILPNLLL	1010
Qy	855	PSLPKKKKKSIVIEHHSHAPATMMQPIOOQL	OOHQHQQOOHQLOOQOOHOOMOOQOO	914
Db	1011	SVLPP-----VIPRASWSAEYMQIPMRRSYT-	FASOPOLEEACLPAQDLINLRLAHQ	1062
Qy	915	QOOHHHRHL--EKRNVSVAQTDDNICGIST	TAGKRSGGDCSMRRRROSTASRHYDSGSQ	972
Db	1063	QATEAKTGLINRLRGIFSRITTSKNKGSLADOKG	--LKAAFKSHMGLFTRLIPS-SQ	1118
Qy	973	TPTARPYSSSHRNSSTNSTSQSELSNMCPHSKP	STPAVLKTPITASDH	1021
Db	1119	TASCNAIYNPNODSIPEASSHPNGHLKPIHRGS	---LTKSGTHLDH	1164
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ID	Q9BML5			
AC	Q9BML5			
DT	01-JUN-2001	(TREMBLrel. 17, Created)		
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)		
DE	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.			
GN	GABA-B-R3.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephyrdoidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[]			
RP	SEQUENCE FROM N.A.			
RA	PubMed=11168554;			
RX	Mexler M., Muller T., Raming K.;			
RT	"Cloning and functional expression of GABA-B receptors from			
RT	Drosophila.";			
RL	Eur. J. Neurosci. 13:477-486(2001).			
KW	EMBL; AF318274; AAK13422.1; -.			
DR	Receptor.			
SK	SEQUENCE	1305 AA; 143701 MW; 8BBFA80F059EADD CRC64;		
Query Match 19.2%; Score 1229; DB 5; Length 1305;				
Best Local Similarity 30.5%; Pred. No. 7.le-80;				
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps				
Qy	48	TGRGVMP-----SVKLAGLVNHGHKITLANYLRLHMWNDOCNAAVGYSFFDMHSG	100	
Db	163	TSRGPREDGISELGATMAVEHINRK-RLLPGTTLELVNTDTCDPGVGDFFHAITYQ	221	
Qy	101	PN--KVMLFGAACHTYTDPIAKASKWHHLTQLSYADTHPMFT-KDAFPNFPRVPSENAF	157	
Db	222	PSTRMVLLGSACEVTESLAKVWPYNNIVQVSFGSTSPALSDDRFEFFYFRTVAPDSSH	281	
Qy	158	NAPRALALKFNTRVGTVQNENPRYSLPHNHWDADLAMEVEVVETQS-FVNDVAESLK	216	
Db	282	NPARIAPIRFKMGTVTFTSONEEVHSAVNNLVTELEANISCAATTFAATDFKEQLL	341	
Qy	217	KLREKDVRIILGNFNEHFARKAFCEAYKLDYGRAYOWLIWATYSTDWNNVTODESCVE	276	
Db	342	LLRETDPRIIIIGSFELAPQILCEAYRLRMFGADYAWILHESMGAPMW-PDQATACSNN	400	
Qy	277	EIAFALEGAILVDLLPLSTSGDITVAGITADELYLVEYDLRGTEYSRPHG-----	326	
Db	401	ELQLAVENLIVSTHNSIVGNVSYGLNNHMF---NSQLR-KOSAOPHGODGEGSGYGP	456	
Qy	327	-----YYDIGWAALAIQYVAE-----	344	

[illegible]

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QY 181 PRYSLPHNHVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFC 240
Db 181 PRYSLPHNHVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFC 240
QY 241 EAYKLDYGRAYOWLIMATYSTDMWNTQDSECSVEEIIATALEGAILVDLLPLSTSGDIT 300
Db 241 EAYKLDYGRAYOWLIMATYSTDMWNTQDSECSVEEIIATALEGAILVDLLPLSTSGDIT 300
QY 301 VAGITADEYLVEYDLRGTEYSRFGHTYDGIWAAALAIQVVAEKREDLLTHFDYRVKDW 360
Db 301 VAGITADEYLVEYDLRGTEYSRFGHTYDGIWAAALAIQVVAEKREDLLTHFDYRVKDW 360
QY 361 ESFLEALRNTSPFGVTPVRFYNNERKANILLINQFQSGMEKIGEXHSOKSHLDLSLGG 420
Db 361 ESFLEALRNTSPFGVTPVRFYNNERKANILLINQFQSGMEKIGEXHSOKSHLDLSLGG 420
QY 421 PVKVGKTPPKDRTLIIYIEHSQVNPITYIVSASASVIGVIIATVFLAFNIKRYNQYIKM 480
Db 421 PVKVGKTPPKDRTLIIYIEHSQVNPITYIVSASASVIGVIIATVFLAFNIKRYNQYIKM 480
QY 481 SSPHLNLIIVGCMITVLSIIFGLDITLSSVAAFPIYICTARAWILMAGFSLSGAMFSK 540
Db 481 SSPHLNLIIVGCMITVLSIIFGLDITLSSVAAFPIYICTARAWILMAGFSLSGAMFSK 540
QY 541 TWRVHSIFTDLKNKKYIKDYQLFMVGVLLAIDIAIITWQIADPPFYRETKQLEPLHHE 600
Db 541 TWRVHSIFTDLKNKKYIKDYQLFMVGVLLAIDIAIITWQIADPPFYRETKQLEPLHHE 600
QY 601 NIDDLVLPENECQSEHMTIFVSIYAYKGLLVFGAFLAWEYRHVSIPALNDSKHGTF 660
Db 601 NIDDLVLPENECQSEHMTIFVSIYAYKGLLVFGAFLAWEYRHVSIPALNDSKHGTF 660
QY 661 SVYNVFITCLAGAAISLVLDKDLVFLVLSFFIIFCTATLCLVFPVKVELKRNPOGV 720
Db 661 SVYNVFITCLAGAAISLVLDKDLVFLVLSFFIIFCTATLCLVFPVKVELKRNPOGV 720
QY 721 VDKRVATLPMKNGRRDSSVCELEQRDLVDKNTNCRFRKALMEKENELQALIRKLGE 780
Db 721 VDKRVATLPMKNGRRDSSVCELEQRDLVDKNTNCRFRKALMEKENELQALIRKLGE 780
QY 781 ARKWIDGVTCTGSGNVGSELEPILDDIVLSAPPVRRMSTVTMTSDVSTSTHVE 840
Db 781 ARKWIDGVTCTGSGNVGSELEPILDDIVLSAPPVRRMSTVTMTSDVSTSTHVE 840
QY 841 MDNSFVSQSVTMAPSLPPKKKQSIYVEHSHAPAPTMQPIQOQLQHQHQHQOQOQ 900
Db 841 MDNSFVSQSVTMAPSLPPKKKQSIYVEHSHAPAPTMQPIQOQLQHQHQHQOQOQ 900
QY 901 LQOQOQHQOQOQOQOQOQOQHHRHLEKRNVSQAOTDNDTIGSITSTAGKRSRGR 960
Db 901 LQOQOQHQOQOQOQOQOQOQHHRHLEKRNVSQAOTDNDTIGSITSTAGKRSRGR 960
QY 961 STASRHYDGSQPTAPRKYSSSHRSNSTNSTSQSELNMCPSKPSPTPAVIKTPTASD 1020
Db 961 STASRHYDGSQPTAPRKYSSSHRSNSTNSTSQSELNMCPSKPSPTPAVIKTPTASD 1020
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Db 1021 HRTSMGSAKSNFVVSQSLDWTHTLSHAKQRSPRNYASQPCAEHGHGHTYDPNT 1080
QY 1081 TSPIQRSVSEKNNKRPKQKGTVCQSETDSEDRERPPPNPQPCVQPRKYSRSSNIQHA 1140
Db 1081 TSPIQRSVSEKNNKRPKQKGTVCQSETDSEDRERPPPNPQPCVQPRKYSRSSNIQHA 1140
QY 1141 AHHSSPNVAPDKQRSQRGKQDSSIIYGASSETELLETGAILIFRKLILTEKSPNYGR 1200
Db 1141 AHHSSPNVAPDKQRSQRGKQDSSIIYGASSETELLETGAILIFRKLILTEKSPNYGR 1200
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Db 1201 SAVGQSCPNIISIKDIVEYL 1220
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RESULT 2
QY133
ID QY133 PRELIMINARY; PRT: 1221 AA.
AC QY133;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BCDNA:GH07312 PROTEIN.
GN GABA-B-R2 OR BCDNA:GH07312 OR CG6706.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley S.E.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Feiraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milghina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Wodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RN Ruben G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA Celniker S.E.;
RT "Full length Drosophila melanogaster cDNA sequence.";
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AE003736; AAF55916.1; -.
DR EMBL: AF145639; AAD38614.1; -.
DR FlyBase: FBgn0027575; GABA-B-R2.
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:00:48 ; Search time 74.36 Seconds
(without alignments)
2399.842 Million cell updates/sec

Title: US-09-715-962-4
Perfect score: 6409
Sequence: 1 MFPSWPFASLLFLLLWST.....SAVQSCPNIKIDIVEYL 1220

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL_17.*
- 1: sp-archaea.*
 - 2: sp-bacteria.*
 - 3: sp-fungi.*
 - 4: sp-human.*
 - 5: sp-invertebrate.*
 - 6: sp-mammal.*
 - 7: sp-mhc.*
 - 8: sp-organelle.*
 - 9: sp-phase.*
 - 10: sp-plant.*
 - 11: sp-rodent.*
 - 12: sp-virus.*
 - 13: sp-vertebrate.*
 - 14: sp-unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6409	100.0	1220	5 Q9BML6	Q9bml6 drosophila
2	6395.5	99.8	1221	5 Q9YL33	Q9yl33 drosophila
3	1229	19.2	1305	5 Q9VPS7	Q9vps7 drosophila
4	1229	19.2	1305	5 Q9BML5	Q9bml5 drosophila
5	1186.5	18.5	840	5 Q9BML7	Q9bml7 drosophila
6	856.5	13.4	816	5 Q9N502	Q9n502 caenorhabdi
7	646.5	10.1	402	5 Q23442	Q23442 caenorhabdi
8	607.5	9.5	1713	5 Q9V309	Q9v3q9 drosophila
9	418	6.5	528	5 Q96954	Q96954 geodia cydo
10	329.5	5.1	153	11 Q9QV85	Q9qy85 rattus norv
11	304	4.7	1188	13 Q98UC5	Q98uc5 gallus gall
12	303	4.7	1242	13 Q98UC4	Q98uc4 gallus gall
13	296	4.6	1156	13 Q98UC6	Q98uc6 gallus gall
14	285.5	4.5	976	5 Q9V485	Q9v485 drosophila
15	281	4.4	983	11 Q62916	Q62916 rattus norv
16	266.5	4.2	738	5 Q9V4U3	Q9v4u3 drosophila
17	265	4.1	1199	11 Q9EPV6	Q9epv6 mus musculu
18	246.5	3.8	941	10 Q9SMD9	Q9smd9 arabidopsis
19	244	3.8	872	4 Q9H3N6	Q9h3n6 homo sapien

20	241	3.8	962	10	O23048	023048 arabidopsis
21	240	3.7	879	11	Q9QYS2	Q9qys2 mus musculu
22	238	3.7	838	5	Q9YOC9	Q9yoc9 dictyosteli
23	237	3.7	921	10	Q9SDQ4	Q9sdq4 arabidopsis
24	237	3.7	923	10	Q9ZV68	Q9zv68 arabidopsis
25	235	3.7	253	5	Q23443	Q23443 caenorhabdi
26	230	3.6	877	13	Q9PW88	Q9pw88 carassius a
27	229.5	3.6	848	13	Q9S553	Q9s553 carassius a
28	228	3.6	1104	13	Q9W6R6	Q9w6r6 fugu rubrip
29	224	3.5	1480	5	Q9V583	Q9v583 drosophila
30	223	3.5	877	4	Q9UGT0	Q9ugt0 homo sapien
31	222	3.5	507	13	Q9DG04	Q9dg04 xenopus lae
32	222	3.5	1267	5	Q93564	Q93564 caenorhabdi
33	221	3.4	1529	5	Q9GQC2	Q9gc2 dictyosteli
34	219.5	3.4	912	10	Q9C561	Q9c561 arabidopsis
35	218.5	3.4	925	10	O65498	O65498 arabidopsis
36	218.5	3.4	2067	11	O9JL19	Q9jl19 mus musculu
37	218	3.4	1920	5	Q9V982	Q9v982 drosophila
38	213.5	3.3	953	10	Q9ZV67	Q9zv67 arabidopsis
39	212	3.3	870	5	Q9N4T8	Q9n4t8 caenorhabdi
40	211	3.3	550	5	Q9VN76	Q9vn76 drosophila
41	210.5	3.3	1010	5	O18346	O18346 drosophila
42	209	3.3	912	10	Q9SES5	Q9ses5 brassica na
43	207	3.2	589	4	Q9UGS9	Q9ugs9 homo sapien
44	207	3.2	853	4	Q9NTG8	Q9ntg8 homo sapien
45	207	3.2	1186	5	Q21227	Q21227 caenorhabdi

ALIGNMENTS

RESULT 1

Q9BML6 ID Q9BML6 PRELIMINARY; PRT; 1220 AA.
AC Q9BML6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE METABOTROPIC GABA-B RECEPTOR SUBTYPE 2.
GN GABA-B-R2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from Drosophila";
RL Eur. J. Neurosci. 13:477-486(2001).
DR EMBL; AF318273; AAK13421.1; -;
KW Receptor.
SQ SEQUENCE 1220 AA; 137976 MW; 2B33DA2C1A1BDA8B CRC64;

Query Match 100.0%; Score 6409; DB 5; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPSWPFASLLFLLLWSTACGRTAKRSVDYIAGFFPYGDVNSYTGRCVMPKSLAL 60

Db 1 MFPSWPFASLLFLLLWSTACGRTAKRSVDYIAGFFPYGDVNSYTGRCVMPKSLAL 60

QY 61 GHVNEHGKILANLYRLHWNNDTCNAAVGVKSFDDMHSGPNKVMFLGAACTHTVDTPIAK 120

Db 61 GHVNEHGKILANLYRLHWNNDTCNAAVGVKSFDDMHSGPNKVMFLGAACTHTVDTPIAK 120

QY 121 ASKHWHLTQLSYADTHPMFTKDAFPNFRVVPSENAFNAPRLALLKEFNWTRVGTVYQNE 180

Db 121 ASKHWHLTQLSYADTHPMFTKDAFPNFRVVPSENAFNAPRLALLKEFNWTRVGTVYQNE 180